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(54) Title: COMPOSITIONS AND METHODS FOR SCREENING DRUG LIBRARIES**(57) Abstract**

A method of screening for binding partners of a specific molecule. The method employs a chimeric protein having at least two different binding regions; one containing at least a portion of the specific molecule or an analog thereof, and the other containing a binding region of an immunoglobulin chain. In a preferred embodiment, the method is used for rapidly screening member compounds of a combinatorial library for potential biological activity.

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DESCRIPTIONCompositions and Methods
for Screening Drug LibrariesField of the Invention

The present invention relates to the fields of chemistry, molecular biology and biochemistry. The invention relates to methods for identifying, from a large
5 collection of random or non-random synthetic molecules, candidates of such molecules able to bind a specific domain of a target molecule. The invention therefore has useful applications in fields including basic biochemical and biomedical research and drug development.

10 Background of the Invention

A significant recent development in pharmaceutical drug discovery and design has been the development of combinatorial chemistry to create chemical libraries of potential new drugs. Chemical libraries are intentionally
15 created collections of different molecules; these molecules can be made by organic synthetic methods or biochemically. In the latter case, the molecules can be made *in vitro* or *in vivo*.

Combinatorial chemistry is a synthetic strategy in
20 which the chemical members of the library are made according to a systematic methodology by the assembly of chemical subunits. Each molecule in the library is thus made up of one or more of these subunits. The chemical subunits may include naturally-occurring or modified amino
25 acids, naturally-occurring or modified nucleotides, naturally-occurring or modified saccharides or other molecules, whether organic or inorganic. Typically, each subunit has at least two reactive groups, permitting the stepwise construction of larger molecules by reacting
30 first one then another reactive group of each subunit to

build successively more complex and potentially diverse molecules.

By creating synthetic conditions whereby a fixed number of individual building blocks, for example, the
5 twenty naturally-occurring amino acids, are made equally available at each step of the synthesis, a very large array or library of compounds can be assembled after even a few steps of the synthesis reaction. Using amino acids as an example, at the first synthetic step the number of
10 resulting compounds (N) is equal to the number of available building blocks, designated as b . In the case of the naturally-occurring amino acids, $b = 20$. In the second step of the synthesis, assuming that each amino acid has an equal opportunity to form a dipeptide with every other
15 amino acid, the number of possible compounds $N = b^2 = 20^2 = 400$.

For successive steps of the synthesis, again assuming random, equally efficient assembly of the building blocks to the resulting compounds of the previous step, $N = b^x$
20 where x equals the number of synthetic assembly steps. Thus it can be seen that for random assembly of only a decapeptide the number of different compounds is 20^{10} or 1.02×10^{13} . Such an extremely large number of different compounds permits the assembly and screening of a large
25 number of diverse candidates for a desired enzymatic, immunological or biological activity.

Biologically synthesized combinatorial libraries have been constructed using techniques of molecular biology in bacteria or bacteriophage particles. For example, U.S.
30 Patents No. 5,270,170 and 5,338,665 to Schatz describe the construction of a recombinant plasmid encoding a fusion protein created through the use of random oligonucleotides inserted into a cloning site of the plasmid. This cloning site is placed within the coding region of a gene encoding
35 a DNA binding protein, such as the lac repressor, so that the specific binding function of the DNA binding protein is not destroyed upon expression of the gene. The plasmid

also contains a nucleotide sequence recognized as a binding site by the DNA binding protein. Thus, upon transformation of a suitable bacterial cell and expression of the fusion protein, the protein will bind the plasmid which produced it. The bacterial cells are then lysed and the fusion proteins assayed for a given biological activity. Moreover, each fusion protein remains associated with the nucleic acid which encoded it; thus through nucleic acid amplification and sequencing of the nucleic acid portion of the protein:plasmid complexes which are selected for further characterization, the precise structure of the candidate compound can be determined. The Schatz patents are incorporated herein by reference.

In other biological systems, for example as described in Goedell et al., U.S. Patent No. 5,223,408, nucleic acid vectors are used wherein a random oligonucleotide is fused to a portion of a gene encoding the transmembrane portion of an integral protein. Upon expression of the fusion protein it is embedded in the outer cell membrane with the random polypeptide portion of the protein facing outward. Thus, in this sort of combinatorial library the compound to be tested is linked to a solid support, i.e., the cell itself. A collection of many different random polypeptides expressed in this way is termed a display library because the cell which produced the protein "displays" the drug on its surface. Since the cell also contains the recombinant vector encoding the random portion of the fusion protein, cells bearing random polypeptides which appear promising in a preliminary screen can be lysed and their vectors extracted for nucleic acid sequencing, deduction of the amino acid sequence of the random portion of the fusion protein, and further study. The Goedell patent is incorporated herein by reference.

Similarly, bacteriophage display libraries have been constructed through cloning random oligonucleotides within a portion of a gene encoding one or more of the phage coat proteins. Upon assembly of the phage particles, the

random polypeptides also face outward for screening. As in the previously described system, the phage particles contain the nucleic acid encoding the fusion protein, so that nucleotide sequence information identifying the drug candidate is linked to the drug itself. Such phage expression libraries are described in, for example, Sawyer et al., 4 *Protein Engineering* 947-53 (1991); Akamatsu et al., 151 *J. Immunol.* 4651-59 (1993), and Dower et al., U.S. Patent No. 5,427,908. These patents and publications are incorporated herein by reference.

While synthesis of combinatorial libraries in living cells has distinct advantages, including the linkage of the compound to be tested with a nucleic acid capable of amplification by the polymerase chain reaction or another nucleic acid amplification method, there are clear disadvantages to using such systems as well. The diversity of a combinatorial library is limited by the number and nature of the building blocks used to construct it; thus modified or R-amino acids or atypical nucleotides may not be able to be used by living cells (or by bacteriophage or virus particles) to synthesize novel peptides and oligonucleotides. There is also a limiting selective process at play in such systems, since compounds having lethal or deleterious activities on the host cell or on bacteriophage infectivity or assembly processes will not be present or may be negatively selected for in the library. Importantly, only peptide or oligonucleotide compounds are made in such systems; thus the diversity of the library is restricted to peptide and polynucleotide macromolecules composed of naturally-occurring monomeric units.

Other approaches to creating molecularly diverse combinatorial libraries employ chemical synthetic methods to make use of atypical or non-biological building blocks in the assembly of the compounds to be tested. Thus, Zuckermann et al., 37 *J. Med. Chem.* 2678-85 (1994), describe the construction of a library using a variety of N-(substituted) glycines for the synthesis of peptide-like

compounds termed "peptiods". The substitutions were chosen to provide a series of aromatic substitutions, a series of hydroxylated side substitutions, and a diverse set of substitutions including branched, amino, and
5 heterocyclic structures. This publication is incorporated by reference herein.

Other workers have used small bi- or multifunctional organic compounds instead of, or in addition to, amino acids for the assembly of libraries or collections
10 compounds of medical or biological interest.

Using chemical synthetic methodologies to create large diverse libraries of potentially useful compounds permits the synthesis of compounds joined to a solid support of some kind. However, the use of such synthetic
15 methods requires the ability, after synthesis, to identify the structure of the rare members of the library which are able to pass a screening process. Thus, such libraries must be rationally designed so as to permit such identification. This task becomes virtually overwhelming as the
20 number of possible compounds grows multiplicatively.

In attempting to consider this latter point, a number of attempts have been made to devise post-screening methods of "addressing" the specific compounds that the screening process indicates as candidates for further
25 study. One class of such addressable libraries employs a strategy of linking the individual peptides of the library with the nucleic acids encoding them. Examples of such systems, such as the use of biological entities such as bacteriophage displaying the compounds of the library or
30 plasmid-binding proteins fused to member compounds of the library have been described above. However, this methodology is not limited to biological systems, and can be employed by the co-polymerization of the test compound and a corresponding nucleotide sequence onto a single solid
35 support.

Another strategy involves chemically synthesizing the combinatorial libraries on solid supports in a methodical

and predetermined fashion, so that the placement of each library member gives information concerning the synthetic structure of that compound. Examples of such methods are described, for example, in Geysen, U.S. Patent No. 5 4,833,092, in which compounds are synthesized on functionalized polyethylene pins designed to fit a 96 well microtiter dish so that the position of the pin gives the researcher information as to the compound's structure. Similarly Hudson et al., PCT Publication No. WO94/05394, 10 describe methods for the construction of combinatorial libraries of biopolymers, such as polypeptides, oligonucleotides and oligosaccharides, on a spatially addressable solid phase plate coated with a functionalized polymer film. In this system the compounds are synthesized 15 and screened directly on the plate. Knowledge of the position of a given compound on the plate yields information concerning the nature and order of building blocks comprising the compound. Similar methods of constructing addressable combinatorial libraries may be used for the 20 synthesis of compounds other than biopolymers.

Another approach has been the use of large numbers of very small derivatized beads, which are divided into as many equal portions as there are different building blocks. In the first step of the synthesis, each of these 25 portions is reacted with a different building block. The beads are then thoroughly mixed and again divided into the same number of equal portions. In the second step of the synthesis each portion, now theoretically containing equal amounts of each building block linked to a bead, is 30 reacted with a different building block. The beads are again mixed and separated, and the process is repeated as desired to yield a large number of different compounds, with each bead containing only one type of compound.

This methodology, termed the "one-bead one-compound" 35 method, yields a mixture of beads with each bead potentially bearing a different compound. Thus, in this method the beads themselves cannot be considered "addressable" in

the same sense as in the solid phase supports and arrays described above, or as in the cellular or phage libraries. However, the compounds displayed in the surface of each bead can be tested for the ability to bind with a specific compound, and, if those (typically) few beads are able to be identified and separated from the other beads, a pre-sumable pure population of compounds can be recovered and analyzed. Of course, this latter possibility depends upon the ability to load and extract enough information concerning the compounds on the surface of each bead to be susceptible to meaningful subsequent analysis. Such information may simply be in the form of an adequate amount of the compound of interest to be able to determine its structure. For example, in the case of a peptide, enough of the peptide must be synthesized on the bead to be able to perform peptide sequencing and obtain the amino acid sequence of the peptide.

For synthetic chemical libraries, not limited to the one-bead one-compound method, in which the compounds of interest are not naturally-occurring peptides or oligonucleotides, analysis can be a tedious and difficult undertaking. In these cases, a code made from easily synthesized and analyzed "tag" molecules (for example, amino acids or other small multifunctional molecules, such as halogenated aromatics) can be co-synthesized with the compounds comprising the library. After a screening procedure, the tag can be "uncoded" to elucidate the structure of the compounds of interest. The code can be relatively arbitrary, so that the structure of any test compound made of building blocks, in which the building block members are able to be designated as corresponding, for example, to an amino acid (or dipeptide, tripeptide etc.), can be determined in this way.

As described above, the construction of combinatorial libraries provides researchers the opportunity to construct a vast number of potential chemical candidates to answer basic and applied structure-function questions,

such as, without limitation: the relationship between a ligand and its receptor, a given antibody and its antigen and an enzyme and substrate. However, the ability to generate large libraries of potential drug compounds
5 overwhelms most available screening methods. Thus, a bottleneck of this emerging and powerful technology remains adequate high-throughput screening procedures to identify the few compounds which are potential candidates for further study from among the thousands, millions or
10 billions of other compounds in the library.

When the combinatorial library is to be screened for the presence of therapeutic or diagnostic agents, candidate compounds are generally initially screened for their ability to bind to a particular member of biological binding partners. By "binding partners" is meant that two or
15 more compounds are able to join under appropriate biological or in vitro conditions to form a specific complex. Examples of such binding partners are, without limitation, antibody and antigen, ligand and receptor, and enzyme and
20 substrate. At times, either ligand or receptor, or both may be comprised of a complex of more than one compound or polypeptide chain. For example, in the case of tumor necrosis factor α (TNF α), the soluble ligand TNF appears to bind to its receptor in the form of a TNF homotrimer;
25 each TNF trimer can bind three copies of the receptor and clustering of the TNF receptor is thought to be required for it to exert its biological effects. Each and all polypeptide chains involved in the binding of the TNF trimer to the clustered receptors are considered
30 individual binding partners.

One common screening method currently applied consists of coating a solid support, such as the wells of a microtiter dish, with the specific molecule for which a binding partner is sought. The library member compounds
35 are then labeled, plated onto the solid support, and allowed to bind the library members. After a wash step, the binding partner complexes are then detected by detec-

tion of the label joined to the bound library members. This type of procedure is particularly well suited to combinatorial libraries wherein the member compounds are provided in a solution or medium. This method can be
5 somewhat labor intensive and, in order to achieve the high throughput required to screen such large numbers of test compounds, may as a first step require screening pools of test compounds, followed by one or more rescreening step
10 in order to specifically identify the compound of interest. The situation can also be reversed, so that the library members are allowed to coat individual wells and are probed with the specific molecule.

In cases wherein the combinatorial library is to contain antibody analogs or peptides targeted to a given
15 epitope, the library members may contain a portion of an antibody recognized by a secondary antibody able to be detected, for example in an enzyme-linked immunological assay (ELISA) or by virtue of being directly or indirectly labeled, for example with a radionuclide, a chemi-
20 luminescent compound, a fluor, and enzyme or dye.

Tawfik et al ., 90 *Proc. Natl. Acad. Sci.* 373-77 (1993) describe a method of screening a library of antibodies (in this case, from a hybridoma library generated using a mimic of the transition state intermediate of an
25 enzymatic reaction) for the presence of rare antibodies having a desired catalytic activity. The screening compound, in this case the enzyme substrate, was immobilized on 96 well microtiter dishes. Supernatants from each clone were placed into separate wells under conditions
30 promoting the enzymatic reaction. The products of the enzymatic reaction, still immobilized to the microtiter dish, were assayed by the use of product-specific monoclonal antibodies. Again, this type of screening process is quite labor-intensive and may necessitate repetitive
35 screening of pools of test compounds in order to achieve high throughput of large libraries.

In the cellular or phage display libraries and "one-bead one-compound" synthetic libraries described above the library members can be screened for the ability to bind a specific binding partner (e.g., a receptor) which is labeled with a detectable fluor, such as fluorescein or phycoerythrin. Because each particle (for example, a cell or a bead) displays only one species of test compound, the fluorescently labeled particles can be detected and sorted using a fluorescence activated cell sorter (FACS). An enriched population of positive beads or particles can then be rescreened, if necessary, and individually analyzed. This strategy can be employed using cells displaying the test compounds or beads on which the test compounds are synthesized. However, this method also suffers from a lack of ease of use, and is time intensive.

Whether screening is by the panning procedure previously described or by binding of labels to the solid phase bound test compounds, a common screening procedure is by competitive binding of the test compounds in the presence of a detectable control ligand, often the natural ligand for the specific binding partner to which the test compounds are intended to be directed. Again, this method can be quite labor-intensive and requires the generation of a standard curve and correlation of the data obtained from the competition experiments with the standard curve in order to generate meaningful data. Thus, competition assays are unable to yield easily interpreted and rapid results in an initial screen of thousands or millions of different library members.

ELISA and similar assay formats are useful when the library members are derivatives of antibodies and contain variable regions directed against known antigens. However, these methods may not be as useful in a non-competitive (i.e., direct) format where neither the specific binding partner nor the desired test compounds are antibodies or contain an available epitope against which a secondary antibody can be easily generated.

Biochemical tools have been generated consisting of chimeric peptides containing portions of a peptide ligand and specific domains of an antibody. Such agents have been devised mainly as therapeutic aids to the delivery of drugs within a patient's body. Especially in the case of peptide drugs, such as soluble agonists of cytokines and other such agents, therapeutic agents or drugs often have a short systemic half-life which reduces the stability of such drugs in vivo. This reduced stability may, in some cases, be counteracted by higher or more frequent dosages, but this may lead to such undesirable consequences as drug tolerance, toxic effects, and high cost of the drug to the patient.

One strategy for overcoming these shortcomings, particularly with regard to the use of systemic biochemical antagonists, has been the use of fusion peptides, which have a longer half life in the circulatory system. These fusion peptides generally contain a binding partner, such as a cytokine receptor, fused to part of an immunoglobulin chain. The immunoglobulin chain acts as molecular camouflage, reducing the opportunity for the binding partner to be recognized as a "foreign" antigen by the organism.

Thus, Shin, et al., 92 *Proc Nat'l Acad. Sci.* 2820-24 (1995) employed fusion peptides made by constructing recombinant vectors having the gene encoding human transferrin fused, in frame, to the 3' end of a chimeric mouse-human IgG3 gene encoding variable and constant regions. The resulting fusion molecules were able to bind antigen (dansyl) and the purified transferrin receptor, and were able to enter the brain parenchyma of rats using the transferrin receptor for transport from the circulatory system. The remaining variable region of the antibody could contain other optional specificities, thus the site is available for secondary targeting of the molecule, such as for therapeutic purposes, once across the blood-brain barrier.

Evans and coworkers, 180 *J. Exp. Med.* 2173-79 (1994), using molecular cloning techniques, reported the construction of a fusion protein containing extracellular portions of the p75 high affinity receptor or, alternatively the
5 p55 low affinity receptor, specific for tissue necrosis factor alpha (TNF α -R) fused to a constant region of human IgG. The soluble, non-fusion forms of the TNF receptors are known to be rapidly degraded in vivo. Cells were transformed with vectors expressing portions of heavy
10 immunoglobulin chain fused to each of TNF receptors. The fusion peptide was more stable than the soluble receptor in serum. Moreover, the fusion peptides were secreted as dimers containing two heavy chains bound by disulfide linkages. The dimers were able to bind the TNF trimers (a
15 naturally-occurring conformation of TNF α) in two separate areas and thus with higher affinity that is possible when the fusion peptide is in the soluble monomeric form.

Other fusion proteins containing a ligand or receptor and an antibody portion have been used in the search for
20 effective therapeutic agonists to humoral agents. In Fountoulakis et al., 270 *J. Biol. Chem.* 3958-64 (1995) the extracellular domain of the human interferon γ receptor was expressed as a fusion protein with the IgG hinge, C μ 2 and C μ 3 domains, and was shown to bind interferon, compete
25 for interferon binding to the cell surface receptor of tissue culture cells, and inhibit interferon-mediated antiviral activity. Due to the immunoglobulin portion of the fusion protein, the protein was expressed in Chinese Hamster ovary cells as a disulfide-linked homodimer. The
30 dimer was able to bind interferon more strongly than the soluble receptor monomer.

In Pitti, et al., 31 *Molec. Immunol.* 1345-51 (1994) the human interleukin-1 (IL-1) receptor was expressed in transfected human cells as a fusion protein containing the
35 hinge and Fc regions of the IgG heavy chain. This fusion peptide was reported to have an extended pharmacological

half-life in the circulatory system of mice and to bind IL-1.

Crowe et al., 168 *J. Immunol. Meth.* 79-89 (1994) expressed a gene containing coding sequences of the extra-
5 cellular domain of the human lymphotoxin α receptor fused to a gene segment encoding the constant portion of human IgG heavy chain. The fusion protein was cloned into a baculovirus vector and expressed in both insect cells and African green monkey kidney cells as a dimer. The IgG
10 portion of the fusion peptide was used as a ligand for affinity purification of the fusion peptide, and also enabled disulfide facilitated dimerization of the fusion peptides to provide a high-affinity ligand for lymphotoxin.

15 These latter five references are incorporated by reference herein.

Summary of the Invention

The present invention is directed to a method of screening candidate biologically active molecules, preferably, though not necessarily contained in combinatorial
20 chemical libraries, in which a multifunctional chimeric protein is constructed and used to directly bind candidate compounds in a screening process for biological activity or binding avidity. The chimeric protein contains at
25 least a portion of a specific binding partner or a peptide analog thereof, with which test compounds are sought to interact. Preferably, the specific binding partner is a ligand or ligand receptor. The chimeric protein also contains at least one portion of an antibody chain which
30 is able to recognize an antigen, able to be recognized as an epitope, and/or which functions as an immunoglobulin hinge domain. In a particularly preferred embodiment the chimeric protein contains an immunoglobulin domain which is able to recognize an antigen and/or able to be recognized
35 as an epitope and also contains the flexible "hinge" region of the immunoglobulin heavy chain placed at a

location between the immunoglobulin portion of the chimeric protein and the receptor moiety. Preferably, the immunoglobulin portion of the chimeric protein is derived from an immunoglobulin heavy chain.

5 Detailed Description of the Invention

Definitions:

By "specific molecule" is meant a molecule such as, without limitation, a ligand; a receptor, such as a cell surface receptor able to bind a ligand; an antibody; an
10 antigen; an enzyme; a hormone; and an enzyme substrate. As will be clear from the specification, the chimeric protein used in the methods of the present invention need not contain all of a specific molecule or its peptide analog, but need only contain enough of a portion to be
15 recognized and bound by a given compound. A specific molecule need not be naturally occurring; it only need be a molecule for whom one or more binding partner is sought to be found.

By "peptide analog" is meant a molecule and
20 resembles, with regard to its binding ability and/or specificity, a specific molecule, as defined above. Such peptide analogs may be found or constructed by protein engineering techniques, such methods being well known to those of skill in the art. Alternatively, such peptide
25 analogs may be found by a reiterative screening process, for example wherein a natural binding partner of the specific molecule (which specific molecule is not necessarily a protein or peptide), or a portion thereof, is used as described herein (i.e. in a chimeric protein) to screen
30 peptide compounds for the ability to bind to it. In a second screening step, the newly found peptide compound (or a portion thereof) may itself be used as a peptide analog of the specific molecule in a chimeric protein to screen for analogs of the natural binding partner. Other
35 methods for finding or making peptide analogs will be apparent to those of skill in the art.

By "epitope" is meant an antigen or portion thereof which is capable of binding with an antibody as an antigenic determinant.

By "binding partner complex" is meant the association
5 of two or more molecules which are bound to each other in a specific, detectable manner; thus the association of ligand and receptor, antibody and antigen, and chimeric protein and the compound to which it binds.

By "chimeric protein" is meant a non naturally-
10 occurring protein or polypeptide comprising some or all of the amino acid sequences from at least two different proteins or polypeptides, or of one protein or polypeptide and a non naturally occurring polypeptide chain. As used herein, a chimeric protein is designed, made, or selected
15 intentionally, and contains at least two domains.

By "directly or indirectly labeled" is meant that a molecule may contain a label moiety which moiety emits a signal which is capable of being detected, such as a radioisotope, a dye, or a fluorescent or chemiluminescent
20 moiety, or may contain a moiety, such as an attached enzyme, ligand such as biotin, enzyme substrate, epitope, or nucleotide sequence which is not itself detected but which, through some additional reaction, is capable of indicating the presence of the compound.

By "secondary molecule" is meant a molecule which is
25 able to bind to a region within the second domain of the chimeric protein, thereby allowing its detection or purification.

By "hinge region" or "immunoglobulin heavy chain
30 hinge region" is meant one of a family of proline and cysteine-containing amino acid sequence regions which occur between the C_H2 and C_H1 regions of many immunoglobulin heavy chains, or analogs of these amino acid sequences based thereon, in which the regions to the amino
35 and carboxy terminal side of the hinge are spatially separated by a turn or kink in the polypeptide chain so as

to facilitate their separate and simultaneous specific binding with other molecules.

By "ligand" is meant a molecule or a multimeric molecular complex which is able to specifically bind another given molecule or molecular complex. Often, though not necessarily, a ligand is soluble while its target is immobilized, such as by an anchor domain imbedded into a cell membrane.

By "receptor" is meant at least a portion of a molecule, or a multimeric molecular complex which has an anchor domain embedded into a cell membrane and is able to bind a given molecule or molecular complex. Many receptors have particularly high affinity for a ligand when either or both the receptor or ligand are in a homo- or heteromultimeric form, such as a dimer.

By "solid support" is meant an insoluble matrix either biological in nature, such as, without limitation, a cell or bacteriophage particle, or synthetic, such as, without limitation, an acrylamide derivative, cellulose, nylon, silica, and magnetized particles, to which soluble molecules may be linked or joined.

By "naturally-occurring" is meant normally found in nature. Although a chemical entity may be naturally occurring in general, it need not be made or derived from natural sources in any specific instance.

By "non naturally-occurring" is meant rarely or never found in nature and/or made using organic synthetic methods.

By "bivalent" is meant able to specifically bind two chemical compounds.

By "multivalent" is meant able to specifically bind two or more chemical compounds.

By "bifunctional" means a compound having two distinct chemical groups capable of separate reaction with one or more additional compound.

By "multifunctional" is meant a compound having two or more distinct chemical groups capable of separate reaction with one or more additional compound.

By "multimeric complex" is meant the stable covalent
5 or non-covalent association of two or more identical or different polypeptide chains to form a structure capable of recognition by a binding partner.

By "modified" is meant non naturally-occurring or altered in a way that deviates from naturally-occurring
10 compounds.

The chimeric protein of the instant invention is useful as a tool in screening a population of compounds for the ability to bind a specific binding partner, at least a portion of said specific binding partner, or a
15 protein or peptide analog thereof, which is comprised in a first binding domain of the chimeric protein. In preferred embodiments the same chimeric molecule also contains a second binding domain comprising at least one immunologically active region (antigenic or antigen-
20 binding) which confers one or more additional binding specificity. This additional specificity may be used as a means for detecting the chimeric protein; for example and without limitation, through the use of a directly or indirectly labeled secondary antibody, or as means for the
25 binding and/or affinity purification of the chimeric protein or compound of interest using, for example, immobilized Protein A or Protein G or an immobilized antibody able to bind the second domain of the chimeric protein. If the second binding domain of the chimeric protein is
30 not derived from an immunoglobulin chain, it may simply comprise a chain of amino acids to which is bound a ligand such as avidin or biotin; however, in such a case the chimeric protein will contain at least a proline-containing hinge region derived from an immunoglobulin chain.

35 While the method of the present invention is particularly useful as a tool for the screening of combinatorial library members, it may be used to screen bacterial or

phage lysates, or in any diagnostic or analytical assay or preparative protocol in which a specific interaction between binding partners is sought to be detected or a compound is sought to be isolated.

- 5 Examples of biochemicals known or thought to exert biological effects by way of specific or semispecific binding to a receptor or binding partner include the following: growth hormone, human growth hormone, bovine growth hormone, parathyroid hormone, thyroxine, insulin A-chain, insulin-B chain, proinsulin, relaxin A-chain, 10 leptin receptor, fibroblast growth factor, relaxin B-chain, prorelaxin, follicle stimulating hormone, thyroid stimulating hormone, luteinizing hormone, glycoprotein hormone receptors, calcitonin, glucagon, factor VIII, an 15 antibody, lung surfactant, urokinase, streptokinase, tissue plasminogen activator, bombesin, factor IX, thrombin, hemopoietic growth factor, tumor necrosis factor alpha, tumor necrosis factor beta, enkephalinase human serum albumin, mullerian-inhibiting substance, 20 gonadotropin-associated peptide, β lactamase, tissue factor protein, inhibitin, activin, vascular endothelial growth factor, integrin receptors, thrombopoietin, protein A or D, rheumatoid factors, NGF- β , platelet growth factor, transforming growth factor, TGF- α , TGF - β , insulin-like 25 growth factor I and II, insulin growth factor binding proteins, CD4, CD8, Dnase, Rnase, latency associated peptide, erythropoietin, osteoinductive factors, interferon-alpha, -beta and -gamma, colony stimulating factors, M-CSF, GM-CSF, G-CSF, stem cell factor, interleukins, IL-1, 30 IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, superoxide dismutase, viral antigens, HIV envelope proteins, gp120, gp140, immunoglobulins, and proteins encoded by the Ig supergene family. These proteins, their ligands or receptors, and fragments or portions of 35 these are included as among potential binding partners contained in the first domain of the chimeric protein.

Thus, in one aspect, the present invention is directed to methods for detecting or isolating a compound comprising contacting the compound with a chimeric protein which contains a first domain comprising a specific binding partner, such as at least a portion of a receptor, antigen, antibody, ligand, enzyme, enzyme substrate or other protein as mentioned above, and a second domain comprising at least one region of an immunoglobulin molecule which is able to specifically bind with an antigen or an antibody, wherein the molecule recognized by the first domain is different than the molecule recognized by the second domain. Preferably, the first domain and the second domain are separated by the proline-containing "hinge" region of an immunoglobulin heavy chain so as to sterically separate the two domains. The chimeric protein is also preferably, though not necessarily, expressed from a vector-borne recombinant DNA molecule containing a nucleotide sequence encoding the chimeric protein. The first domain may be situated either to the amino terminal side or the carboxy terminal side of the second domain; in a particularly preferred embodiment the chimeric protein has the first domain situated to the amino terminal side of the second domain.

In this aspect of the invention the compound of interest, if present, will bind to a region within the first domain of the chimeric protein. If the compound is immobilized, such as in a cellular or phage display library or in the "one-bead, one-compound" libraries, the solid support can then be washed free of excess chimeric protein and the chimeric protein:compound conjugate (binding partner complex) detected. In a preferred embodiment, the chimeric protein is detected by binding the second domain of the chimeric protein with a labeled secondary binding partner, such as a enzyme-labeled anti-IgG secondary antibody, specific for a region of the second domain. Detection of the secondary antibody permits identification of solid supports containing compounds which are able to

interact with the binding partner of the first domain. These compounds can then be analyzed for elucidation of their structure or in additional assay protocols.

In this preferred embodiment, if the labeled secondary binding partner used to bind the second domain has a fluorescent or pigmented label or contains a moiety that participates in a reaction to form a fluorescent or pigmented product, the candidate compounds linked to solid supports can be separated from non-candidate (i.e., non-binding) compounds using a cell sorter; such instruments, such as fluorescent-activated cell sorters (FACS), are well known in the art. After sorting, individual solid supports can be isolated, the chimeric protein eluted from the bound compound of interest, and the compound characterized. Alternatively, for solid supports containing a tag identifying the immobilized compound, the tag may be "read" to obtain information about the compound. Solid supports may also be sorted by hand, provided the particle is large enough to be so manipulated.

The secondary binding partner may alternatively be joined to a solid support, such as a magnetic sphere to facilitate purification of the binding partner complex. In such a case, application of a magnetic field will allow the beads to be washed free of unbound compounds prior to isolation and purification. Such a strategy may be employed even when the library members are themselves bound to a solid support.

In another aspect, the chimeric protein may be immobilized on a solid support in such a way as to allow binding of the binding partner of the first domain with a compound in solution. Immobilization may be performed by formation of an antibody:antigen binding complex partner between the solid support (e.g., with an anti-IgG antibody covalently joined thereto, or through use of Protein G or Protein A) and the variable region or antigenic epitope of the second domain of the chimeric protein. After contacting the immobilized chimeric protein with a sample

suspected of containing one or more compound of interest, other components of the sample may be washed away and the compound(s) then eluted to produce an enriched population of candidate compounds.

5 In yet another aspect, the present invention is directed to diagnostic assay methods for the detection or quantification of a member of a binding pair, for example, a receptor, cytokine, enzyme, antibody, ligand or the like, in a sample. The method includes contacting a chi-
10 meric protein, as described above, with a sample suspected of containing the compound of interest under conditions permitting the binding of the first domain of the chimeric protein and the compound. Preferably, the compound is immobilized on a solid support so that a chimeric protein:
15 compound binding partner complex is formed after said contacting step. The solid support-bound binding complex can then be washed and the complex detected by interaction of the second domain of the chimeric protein with a directly or indirectly labeled ligand, such as a secondary
20 antibody.

In yet another aspect, the invention is directed to methods for rapidly screening members of a chemical combinatorial library. The library members may be contained in solution or may be immobilized on solid phase supports,
25 whether synthetic or biological. The compounds to be screened may be peptides, oligonucleotides, saccharides, mixtures or analogs of any of these molecular types, other organic molecules, or non-organic compounds which are desired to be preliminarily screened on the basis of their
30 interaction with a binding partner. The relationship between the binding partner and the compound to be screened may be, for example, antibody:antigen, ligand:receptor, enzyme:substrate or any other specific binding interaction between a protein binding partner and a
35 compound. It will be understood that such methods may be used to screen and aid in the identification of analogs and non-naturally-occurring mimics or variants of the

natural ligands of these binding partners. Additionally, the specific binding partner contained in the chimeric protein need not be a natural ligand but may itself be an analog of a naturally-occurring ligand.

- 5 In this aspect of the invention, the members of the combinatorial library are contacted with the chimeric protein under conditions favoring the binding of the binding partner contained in the first domain of the chimeric protein with a ligand. It is preferred that the
- 10 chimeric protein be joined to at least another chimeric protein, either identical or different, to form a multimer, most preferably a dimer, joined together, for example, one or more disulfide linkage. In this form, the chimeric protein is at least bivalent with respect to the
- 15 specific binding partner of the first domain and therefore may have the potential to bind a given compound at more than one location, and more strongly than the monomeric form or which the solid support containing monomeric compounds closely packed on the surface of the support.
- 20 This is particularly true when the compound itself is in multimeric form. Use of chimeric proteins in multimeric form can be of particular advantage in detecting the presence of low- or medium-affinity candidate compounds from within the library; these compounds may have a
- 25 completely different structure than the high affinity compounds, and elucidation of alternative ligand structures may yield information valuable in the later design of diverse higher affinity ligands with different chemical, biochemical or physical characteristics.
- 30 The chimeric protein can then be used to isolate or detect the library members to which it has bound through a second domain of the chimeric protein comprising at least one region of an immunoglobulin molecule which is able to specifically bind with an antigen or an antibody,
- 35 wherein the molecule recognized by the first domain is different than the molecule recognized by the second domain. If the members of the combinatorial library are

joined to a solid support, the solid support can be washed free of any unbound chimeric protein and the second domain of the specifically bound chimeric protein molecules allowed to bind with a labeled binding partner, such as a
5 fluorescently, enzyme-labeled radioactively, or dye-labeled secondary antibody. Subsequent detection of the label-associated solid support particles permits identification and isolation of the compound of interest.

It will be apparent in light of the instant disclosure, that, if the compounds being screened are
10 peptides, a chimeric protein can be made having a first domain including a known peptide, for example, the extracellular portion of a cell surface receptor for a specific humoral factor. If analogs to the cell surface receptor
15 are desired, one may employ the methods disclosed herein to isolate compounds from a peptide combinatorial library able to bind the receptor. Upon determination of the structure of such a compound, this new compound can be made the "binding partner" portion of the first domain of
20 a new chimeric protein, and the new chimeric protein used to screen the same or a different combinatorial library for analogs of the receptor. It will also be apparent that this method may be employed to obtain "binding analogs" of a given compound even when the structure of
25 the natural binding partner for a given compound is not known.

Thus, another aspect of the present invention is a method of making a chimeric protein useful in the screening of compounds for their ability to bind a given peptide, comprising the construction of a recombinant plasmid
30 containing a nucleotide sequence encoding at least one constant (C) or variable (V) region of an immunoglobulin chain positioned downstream from a promoter sequence. While it is preferred that the portion of the gene encoding the immunoglobulin chain correspond to either the
35 amino terminal region or the carboxy terminal region of the mature immunoglobulin molecule, all that is necessary

is that the nucleotide sequence encode a portion of at least one C or V region recognizable by an antigen or antibody. The portion of the nucleotide sequence encoding the immunoglobulin (C) and/or (V) region have a region at
5 either its 3' or 5' end one or more restriction endonuclease sites for insertion of a DNA fragment within the coding sequence preferably, the region contains a restriction cluster of about four or more different restriction endonuclease cleavage sequences for facile cloning. If
10 this restriction cluster is located at the 5' side of the immunoglobulin sequences, the restriction cluster must be positioned between the immunoglobulin sequences and the promoter sequence. Also, the cloned immunoglobulin chain portion preferably contains the nucleotide sequence encoding the "hinge" region of an immunoglobulin chain; such a
15 region usually comprises a proline-containing region having at least one cysteine residue. It will be understood that reference to the 3' or 5' side of a particular nucleotide sequence or sequence region refers to the coding strand of the DNA molecule unless indicated otherwise
20 herein. Preferably, the immunoglobulin chain contains sequences derived from an immunoglobulin heavy (H) chain which include constant (C) region nucleotide sequences.

Such a vector can be regarded as a "cassette holder";
25 that is this portion of the vector is capable of receiving many interchangeable nucleic acid fragments ("cassettes") encoding portions of receptors, ligands, or other binding partners. The fragments should be engineered or selected to contain restriction sites matching those at one end of
30 the immunoglobulin sequences; in such a case, ligating the binding partner fragment into the vector is trivial. Care must be taken, however, to ensure that the binding partner gene fragment ("cassette") is placed in the same reading frame as the immunoglobulin portion of the chimeric gene.
35 This can be accomplished, if necessary through the construction and use of appropriate oligonucleotide primers or linkers containing a number of bases sufficient to

place the cassette in the same reading frame as the immunoglobulin portion of the chimeric gene. If desired, one or more of the primers or linkers may also be constructed to incorporate nucleotide sequences comprising one or more restriction endonuclease cleavage site for facile cloning and interchange of subunits of the binding partner.

Suitable cassettes can be easily constructed; as an example by using PCR or another nucleic acid amplification method. Such methods generally utilize at least two primers directed to different strands and to different locations 5' and 3' (with respect to the coding strand) of the gene portion to be cloned. When the gene fragment, encoding, for example, a portion of a receptor molecule is to be cloned at the 5' end of the gene, the 5' portion of the nucleic acid to be amplified will generally contain an ATG start codon. An example of such a primer is shown in the Examples below. Such a primer can also be directed to the untranslated region of the gene 5' of the ATG to be amplified, in order to ensure that other transcription or translation regulatory sequences (such as the TATA box or a ribosomal binding sequence (RBS)) are also included in the amplified nucleic acid. An example of a consensus eukaryotic RBS is: SEQ ID NO: 19; 5'-GCCRCCATGG-3', where "R" is either A or G. The primer may be directed to sequences to the 5' side of such regulatory sequences, may be directed to some or all of such sequences themselves, or may not be designed to amplify such sequences at all. Those of skill in the art will, in light of this disclosure, recognize that for a given binding partner one of these options may optimize the expression of the chimeric gene; determination of which of these three options may be optimal is a matter of routine screening easily performed by those of skill in the art.

The recombinant vector is preferably capable of replication and expression of the chimeric protein in eukaryotic cells; thus the vector will preferably contain

an origin of replication allowing the episomal replication in such cells. In such a case, the promoter directly upstream from the cloned synthetic gene encoding the chimeric protein will be one capable of directing transcription in a eukaryotic host. It is also preferable that the vector and host cell be chosen so as to allow the vector to be replicated and transcribed at high copy number by the eukaryotic cell.

Expression of such chimeric proteins in eukaryotic cells allows the cell to treat the expressed chimeric protein much like an immunoglobulin molecule. Thus, the chimeric protein may be glycosylated, permitted to form dimers or other multimeric forms and transported to the cell surface for secretion just as a native immunoglobulin would. This also allows the chimeric protein to be harvested from the tissue culture supernatant without lysing the cells, therefore facilitating purification. As described below, Applicant has demonstrated the feasibility of this approach by cloning and expressing the chimeric protein as a secreted product in African green monkey cells.

Purification of the chimeric protein can be performed by exploiting one of the two specific binding domains of the chimeric protein in a minimum of steps by affinity chromatography; for example, by lysed anti-IgG antibody. The chimeric protein can then be eluted from the affinity matrix for use. Alternatively, the cell-free tissue culture medium containing the chimeric protein can be used without further purification.

In embodiments of the invention employing non-biological solid supports, these solid supports are any insoluble or semisoluble matrix on which chemical compounds, including antibodies and other proteins and members of a combinatorial library, can be joined. Such matrices include: nitrocellulose; cellulose derivatives; nylon; controlled pore glass; polystyrene or polyacryl-

amide derivatives; dendromeres, magnetic beads; particles or microspheres.

Additional embodiments of the present invention are directed to methods of using the chimeric proteins described herein. One such method of use - that of utilizing the first domain of the chimeric protein to bind solid supports displaying a compound or library member of interest, identifying the bound chimeric protein by directing a labeled ligand to the second domain of the protein, detecting the label, and sorting the identified solid supports - has been described above. The chimeric protein may also be used in an application in which the candidate compounds are coated onto a microtiter well, the chimeric protein added, and a directly or indirectly labeled ligand directed to the second chimeric protein domain used to identify the bound chimeric protein. An example of indirectly labeled ligands are antibodies labeled with an enzyme, such as horseradish peroxidase or alkaline phosphatase, which can then be exposed to a substrate in a colorimetric reaction to indicate the presence of the compound of interest. The converse of this scheme may also be employed in which the chimeric protein is immobilized and the library members are used to bind thereto. In the interests of increased assay throughput, an initial screen can be performed using mixtures of different compounds, and subsequent screens can then identify the specific compounds of interest.

Additional embodiments can be found in the examples and in the claims which conclude this specification.

30 Examples

Example 1: Vector Construction

The commercially available vector pcDNA3 was purchased from Invitrogen Corp., San Diego CA. This eukaryotic/prokaryotic shuttle vector, which is 5.4 kb in length, includes the following elements: the cytomegalovirus (CMV) eukaryotic promoter and the T7 bacteriophage

promoter, both promoting transcription in the clockwise direction; the SP6 bacteriophage promoter, promoting transcription in the opposite direction; a polylinker containing restriction sites for, in order from 5' to 3' with respect to the cloned sequences described below, :
5 Hind III, Kpn I, Bam HI, BstX I, EcoR I, EcoR V, BstX I, Not I, XhoI, Xba I and Apa I; the SV40 eukaryotic origin of replication, the ColE1 bacterial episomal origin of replication, the ampicillin resistance gene, and the
10 neomycin resistance gene.

This plasmid was linearized using the restriction enzymes Not I and Xho I, as follows. A 200 μ l reaction mixture containing 30 (New England Biolabs), 10 mM Tris HCl (pH 7.9), 10 mM $MgCl_2$, 50 mM NaCl, 1 mM DTT and
15 100 μ g/ml BSA (bovine serum albumin) was incubated at 37 °C overnight. The DNA fragments were separated on a 1% agarose gel using TBE (89 mM Tris (pH 8.0), 89 mM boric acid, 2 mM EDTA (ethylene diamine tetraacetic acid)). The large linearized DNA fragment was excised from the gel,
20 the gel slice crushed and the DNA extracted by adsorption on glass particles, and purified by precipitation in ethanol. The purified DNA fragment was resuspended in TE (10 mM Tris (pH 7.5, 1 mM EDTA), and the concentration of the purified DNA fragment ascertained by determining the
25 absorbance of the solution at 260 nm in a spectrophotometer. The isolated DNA was stored at -20 °C until use.

Genomic mouse DNA was prepared from a lysate of frozen NIH3T3 cells (a mouse fibroblast cell line. An aliquot of NIH3T3 cells (5×10^5) were centrifuged at 2500 xg
30 for 4 minutes and washed three times with PBS (phosphate-buffered saline). The cells were resuspended in 100 μ l of a hypotonic buffer (50 mM KCl, 10 mM Tris HCl (pH 8.4), 1.5 mM $MgCl_2$) containing 0.5% (v/v) TWEEN® 20 nonionic surfactant and 10 μ g of proteinase K, and incubated at 56
35 °C for 45 minutes. The crude lysate was then incubated at 95 °C for 10 minutes, and finally stored at 4 °C.

Cloning of the IgG1 Immunoglobulin Fragment

The carboxy-terminal mouse DNA sequences encoding the constant region C_H2, C_H3 and hinge domains of the murine IgG1 heavy chain were amplified from NIH3T3 genomic DNA using PCR. The following oligonucleotide primers were synthesized to be complementary to corresponding portions of the immunoglobulin gene. The underlined portion of SEQ ID NO. 1 corresponds to a Not I restriction endonuclease cleavage site, and the bolded underlined portion of SEQ ID NO. 2 corresponds to an Xho I restriction endonuclease cleavage site.

Sense primer (SEQ ID NO. 1):

5'-- AGCTTCGAGC GGCCGCCGTG CCCAGGGATT GTGGTTGTAA G--3'

Antisense primer (SEQ ID NO. 2):

15 5'--GATCCTCGAG TCATTACCA GGAGAGTGGG AGAGGCT--3'

The PCR reaction was set up by adding the following reagents to a sterile 0.6 ml microfuge tube in the following order: ten microliters of 10X PCR Buffer II (100 mM Tris HCl (pH 8.3), 500 mM KCl), 6 μ l of 25 mM MgCl₂, 2 μ l of a 10 mM solution of each dNTP, 2.5 μ l of 10 μ M mouse IgG1 sense primer (SEQ ID NO. 1), 2.5 μ l of 10 μ M mouse IgG1 antisense primer (SEQ ID NO. 2), 0.5 μ l (2.5 units) of AMPLITAQ[®] thermostable DNA polymerase (Perkin Elmer Corp.), 66.5 μ l ultra pure water, and one wax bead. The reaction mixture was incubated at 70°C until the wax bead melted, then 10 μ l of the NIH3T3 lysate was added. The reaction mixture was placed in a Perkin Elmer 480 Thermal Cyclor, and the cyclor programmed to run 30 cycles under the following conditions: 1 minute at 94 °C, 55 °C for 1 minute, 72 °C for 1.5 minutes, and held at 4 °C until use.

The amplified DNA from the PCR reaction was gel purified by electrophoresis through a 1% agarose gel in TBE. The DNA band corresponding to the amplified DNA was excised from the gel, and eluted in 40 μ l of water as

above. The purified amplified IgG1 gene fragment was then digested with the restriction enzymes Not I and Xho I as described above. The restriction digest was run on a 1% agarose/TBE gel, the approximately 1 kb fragment was excised from the gel and the DNA eluted from the gel slice in 40 μ l of water. The yield was determined by measuring the optical density of the solution at 260 nm on a Beckman DU600 spectrophotometer.

The Xho I- and Not I-digested IgG1 PCR product was ligated into the Xho I- and Not I- digested pcDNA3 vector as follows. The ligation reaction was performed in a total volume of 20 μ l containing approximately 100 ng pcDNA3 and 100 ng of the IgG1 PCR fragment. This was incubated in 50 mM Tris-HCl (pH 7.8), 10 mM MgCl₂, 10 mM DTT, 1 mM ATP, 25 μ g/mL BSA with 1 unit of DNA ligase at room temperature overnight.

A 1 μ l aliquot of the ligation mix was used to transform Stratagene Epicurean Coli SURE[®] Competent Cells (these cells have the genotype: e14-(McrA-) Δ (mcrCB-hsdSMR-mrr)171 endA1 supE44 thi-1 gyrA96 relA1 lac recB recJ sbcC umuC::Tn5 (Kan^r) uvrC [F' proAB lacI^qZ Δ M15 Tn10 (Tet^r)] and are supplied in a transformation buffer). A 50 μ l aliquot of thawed cells was placed on ice with 1 μ l of the ligation reaction mixture for 30 minutes, followed by a heat shock at 42°C for 45 seconds. 500 μ l of Luria broth was added and the cells incubated at 37°C for 1 hour with shaking. The transformants were plated onto LB (Luria broth plates containing 50 μ g/mL ampicillin; pcDNA3 carries the β -lactamase gene, which confers resistance to ampicillin whereas untransformed cells do not contain this gene. Representative transformants were used for the preparation of vector DNA by standard "miniprep" procedures, as described in Sambrook et al., *Molecular Cloning: A Laboratory Manual* (Cold Spring Harbor Press 2d ed. 1989).

Vector DNA was digested with Not I and Xho I and resolved on a 1% agarose/TBE analytical gel to check for

the presence of the cloned, PCR-derived mouse IgG1 constant and hinge region. Vector DNA from clones containing Not I/Xho I inserts was purified as described above prior to nucleic acid sequencing.

5 Nucleic acid sequencing was performed using Applied Biosystems' PRISM[®] Dye Terminator Cycle Sequencing Ready Reaction Kit according to the manufacturer's instructions. This protocol employs fluorescently-labeled dideoxyribonucleotides as chain terminators for the sequencing
10 reaction, and the results are automatically recorded. The sequencing reaction mixtures were run on a 4% acrylamide denaturing gels containing urea for 10 hours and the entire sequence of the fragment determined. After verification that a clone contained the proper sequence, a
15 large-scale vector preparation was done. The new vector, containing the mouse IgG1 C_H2, C_H3, and hinge regions, was termed pcDNA3-IgG1, disclosed herein as SEQ ID NO: 5. It will be recognized that this vector may be used to clone DNA fragments whose 3' end incorporate a Not I restriction
20 endonuclease site.

Applicant has also found that a corresponding segment of the IgG2b heavy chain containing the C_H2, C_H3, and hinge regions can be cloned in a similar manner. These IgG2b chimeric proteins may be preferable for certain
25 applications.

Since the primary structure of many immunoglobulins is known, it will be clear to those of skill in the art that a similar strategy may be employed to clone DNA fragments encoding receptors and other peptide binding
30 partners at a position 3' (rather than 5', as above) to the immunoglobulin-encoding portion of the chimeric gene. Upon expression, the result would be a chimeric protein containing the binding partner at its carboxy terminus. This conformation not only would allow the possibility of
35 presenting the binding partner to the test or library compounds in both amino- and carboxy-oriented aspects, but provides the possibility of including a desired variable

region of an immunoglobulin chain, for example a monoclonal antibody, as part of the second domain of the chimeric protein. Moreover, if the V_H , and at least the C_H2 , C_H3 immunoglobulin regions and the binding partner
5 were included in the chimeric protein, it would be reasonably expected in light of the present disclosure that such a chimeric protein might not only have one specific binding region within the second domain, but may in fact have two.

10 Cloning of tumor necrosis factor receptor (TNF-R) into pcDNA 3-IgG1

The DNA fragment encoding the extracellular portion of the human tumor necrosis factor- α receptor (TNF-R) was obtained from PCR amplification of total RNA cDNA from
15 human peripheral blood mononuclear cells (PBMC). RNA was collected from the PBMCs using standard procedures. The RNA was reverse transcribed in a reaction mixture containing 1 μ g PBMC whole RNA, 12.5 mM each dNTP, 50 mM Tris-HCl (pH 8.3), 40 mM KCl, 5 mM DTT (dithiothreitol), 20 pmoles
20 of a random deoxyribonucleotide hexamer, and 100 units SUPERScript[®] reverse transcriptase. The reaction mixture was incubated at 42°C for 1 hour, then at 95°C for 5 minutes, and stored at 4°C until use.

PCR reactions of the PBMC cDNA preparation were
25 performed using the following primers.

TNF-R sense primer (SEQ ID NO. 3):

5'--GATCGGATCC ATGGGCCTCT CCACCGTGCC TGAC --3'

TNF-R antisense primer (SEQ ID NO. 4):

5'--AGCTTCGAGC GGCCGCTGTG GTGCCTGAGT CCTCAGTGCC--3'

30 The primer having SEQ ID NO: 3 incorporates a ATG start codon (underlined) and a Bam HI site (bolded) into the amplified nucleic acid.

PCR reactions were performed as described previously. The TNF-R PCR product and the pcDNA3-IgG1 were each digested with BamHI and Not I, and the larger DNA fragments of each reaction were gel purified as described
5 above. The purified TNF-R DNA fragment and vector fragment were then ligated together as described above to yield the chimeric protein expression vector pcDNA3-IgG1-TNF-R, disclosed herein as SEQ ID NO: 6, having the TNF-R fragment in the proper orientation. Vector construction
10 was confirmed by diagnostic restriction digestion and nucleic acid sequencing. Large scale vector preparations were made from the transformed E. coli clone.

Example 2: Transfection of African green monkey cells with pcDNA3-IgG1-TNF-R, and expression of the chimeric protein.

15 The host cells chosen to demonstrate expression of the chimeric protein of the present invention were COS-7 African green monkey kidney cells. This cell line can be used for large scale production of heterologous proteins by transfection and expression of a recombinant vector
20 having appropriate regulatory elements, such as pcDNA3-IgG1-TNF-R.

COS-7 cells were grown in Dulbecco's Modified Eagle Medium supplemented with 4500 mg/nl D glucose, 584 mg/ml L-glutamine, and 10% fetal bovine serum (FBS). For
25 transformations, cells were seeded at $1-2 \times 10^5$ cells/ml and incubated at 37°C at 5% CO₂ until 50-70% confluent. By percentage confluent is meant the percentage of the substrate, such as the microtiter dish bottom, that is occupied by cells. The cells were then transfected as
30 follows. For each transfection a solution was made by mixing 20 μ l LIPOFECTIN[®] (a cationic lipid preparation containing a 1:1 molar ratio of DOTMA (N-[1-(2-, 3-dioleoyloxy) propyl]-N,N,N trimethylammonium chloride) and DOPE (dioleoyl phosphatidylethanolamine) with 100 μ l serum-
35 free medium and the solution was allowed to stand at room temperature for 30 minutes. One to two microliters of the

pcDNA3-IgG1-TNF-R solution was also diluted into 100 μ l serum-free emdium. The two solutions were combined, mixed gently and incubated at room temperture for 10-15 minutes. Cells were then overlayed with the DNA-LIPOFECTIN[®] mixture and incubated overnight at 37°C. Trasfection mixture was then removed and replaced with medium. Expression of the pcDNA-IgG1-TNF-R vector was constitutive in the COS-7 cells. The chimeric protein is secreted into the culture media, and can be harvested by decanting or aspirating the cell-free media. Cell-free supernatant was assayed for secretion of the chimeric protein at 48-72 hours following transfection.

Example 3: Screening of compounds coated within microtiter wells using an immunoglobulin-binding partner chimeric protein.

Following expression of the chimeric protein, the cell-free culture medium was harvested and tested for the presence of the fusion protein. The wells of a plastic microtiter dish were coated with a preparation of TNF α by addition of 2 ng of recombinant TNF α per well in PBS and overnight incubation at 4°C or 2 hours at room temperature. The wells were then washed three times with wash buffer (PBS containing 0.05% (v/v) TWEEN[®]-20 non-ionic detergent. Following the wash, the wells were blocked to prevent non-specific binding with PBS containing 1% (w/v) BSA and 0.05% TWEEN[®]-20 non ionic detergent (blocking buffer). The wells were again washed as before. The culture media was serially diluted two-fold 11 times in the blocking buffer and 50 μ l of each dilution (and the undiluted media) was added to the coated, blocked wells. A set of uncoated wells also received the diluted cell-free media. Microtiter plates were then incubated for 2 hours at room temperature, then washed three times as before. The presence of the bound chimeric protein was assayed using 100 μ l of a 1:5000 dilution of an anti-mouse IgG antibody labeled with horseradish peroxidase (ELISA).

Color development was commenced with addition of 100 μ l of a commercially obtained chromogenic horseradish peroxidase (HRP) substrate (TMB Color Reagent, Kurkegaard & Perry Laboratories) to each of the microtiter wells.

5 The plates were incubated at room temperature for up to 20 minutes. Color development in this assay system may be terminated by addition of 100 microliters of a stop solution (Kirkegaard & Perry, product code 50-85-05) to each well.

10 The control wells showed no color development. By contrast, the wells in which a TNF/TNF-R complex had been formed showed a distinct blue to purple color formation. The absorbance of each dilution at 450 nm was measured, the absorbance at 650 nm was subtracted, and the results

15 were plotted. The results are shown below.

Dilution	1:1	1:2	1:4	1:8	1:16	1:32	1:64	1:128	1:256	1:512	1:1024	1:2048
Transfected medium	1.147	1.199	1.161	0.901	0.747	0.406	0.259	0.166	0.112	0.085	0.071	0.037
Untransfected Medium	0.101	0.028	0.028	0.053	0.037	0.055	0.053	0.0764	0.044	0.063	0.075	0.057
No TNF Control	0.136	0.032	0.030	0.035	0.038	0.035	0.029	0.023	0.028	0.027	0.029	0.040

The results indicate that neither the control wells containing tissue culture media from untransfected cells,

25 nor the control wells containing the media from transfected cells in the absence of TNF gave an indication of color formation; i.e. specific binding between the chimeric protein and the TNF binding partner. However, the media from cells transfected with the vector encoding

30 the chimeric protein was able to bind to wells coated with TNF, and gave a titration curve indicating the presence of specific target binding.

Example 4: Screening of particle-bound compounds using an immunoglobulin-binding partner chimeric protein.

Recombinant TNF α (obtained from R & D Systems) was immobilized on cyanogen bromide-activated SEPHAROSE[®] CL 4B agarose beads as follows. A 0.5 ml aliquot of cyanogen bromide-activated SEPHAROSE[®] 4B was washed with ice-cold 0.1 N HCl. Ten micrograms of TNF α were dissolved in 10 μ l PBS, then added to 100 μ l of a solution of 0.1 M HCO₃ and 0.5 M NaCl. This was mixed with 100 μ l of the washed, activated SEPHAROSE[®] beads and the suspension incubated at room temperature for 2 hours.

The unreacted cyanogen bromide-activated sites were blocked by the addition of 500 μ l of 50 mM glycine (pH 8.0) to the TNF-coupled SEPHAROSE[®] beads. The same amount of the glycine solution was added to 100 μ l of washed, uncoupled SEPHAROSE[®] as a negative control.

Potential sites of non-specific binding of protein to the SEPHAROSE[®] beads was blocked by resuspending and incubating the two bead slurries (TNF and control) in 10 volumes of 1% (w/v) BSA and in TBST (20 mM Tris-HCl (pH 7.5), 150 mM NaCl and 0.05% (v/v) TWEEN[®] 80 non-ionic surfactant) for 15 minutes at room temperature.

Forty microliters of the TNF and control SEPHAROSE[®] beads were each exposed to 100 μ l of tissue culture supernatant from either untransfected or the pCDNA3-IgG1-TNF-R transformed COS-7 cells and incubated at room temperature for 1 hour. The beads were then washed with TBST.

Detection of the bound chimeric protein was accomplished through the use of a secondary anti-mouse IgG1 antibody coupled to alkaline phosphatase (AP). The alkaline phosphatase-coupled antibody, and its chromogenic substrate was obtained from a commercially available kit, the PROTOBLOT[®] II AP System (Promega Corp.), and used in accordance with the manufacturer's directions. A solution of AP-anti-mouse IgG (1mg/ml) was diluted 1:5000 into Tris-buffered saline (TBS; 20 mM Tris-HCl (pH 7.5), 150 mM NaCl). One hundred microliters of this solution was added

to the aliquots of SEPHAROSE® beads and incubated at room temperature for 1 hour. The beads were then washed three times in TBS.

Color development was commenced with addition of 100
5 μ l WESTERN BLUE® chromogenic AP substrate to each of the
aliquots of SEPHAROSE® beads. These were incubated at room
temperature for 20 minutes. Color development in this
assay system may be terminated by washing the beads with
water. Aliquots of each SEPHAROSE® bead mixture were
10 observed under a microscope using a 10 X objective lens.
The control beads remained colorless. By contrast, the
beads in which a TNF/TNF-R complex had been formed were
stained with a distinct blue to purple color.

Example 5: Construction of Additional Fusion Peptides

15 Using the pCDNA3-IgG1 "cassette holder" and the same
strategy employed in the Examples described above, addi-
tional individual chimeric proteins were made having, at
the amino terminal regions, extracellular ligand-binding
portions of the erythropoietin receptor, FAS (a receptor
20 of the Nerve Growth Factor family having properties
similar to TNF α -R), the interleukin 4 receptor, and the
interleukin 6 receptor. The nucleotide sequences for
these receptors was obtained from the GENBANK nucleotide
sequence database. The nucleotide sequences of other
25 binding partners can be obtained from published or data-
base sources, or can be obtained by direct peptide
sequencing of an isolated protein.

Primers designed to amplify the extracellular
portions of the indicated receptors were employed to
30 obtain PCR-amplified, "clonable" double-stranded DNA. As
above, sense primers incorporated a BamH1 site just prior
to the ATG initiation codon, and antisense primers
incorporated a Not 1 restriction site after the termination
codon. Primer sets (with the initiation codon of the
35 sense strand underlined) and the amplified DNA sequences
(coding strand sequence only) were as follows :

Erythropoietin ReceptorSense primerSEQ ID NO: 7

5' -GATCGGATCCATGGACCACCTCGGGGCGTCCCTC-3'

5 Antisense primerSEQ ID NO: 8

5' -AGCTTCGAGCGGCCGCGGGGTCCAGGTCGCTAGGCGTCAG-3'

EPO Receptor DNA sequence amplified:SEQ ID NO: 9

10 5' -ATGGACCACCTCGGGGCGTCCCTCTGGCCCCAGGTCGGCTCCCTTTGTCTCCT
GCTCGCTGGGGCCGCCTGGGCGCCCCCGCCTAACCTCCCGGACCCCAAGTTCGAGA
GCAAAGCGGCCTTGCTGGCGGCCCGGGGGCCCGAAGAGCTTCTGTGCTTCACCGAG
CGGTTGGAGGACTTGGTGTGTTTCTGGGAGGAAGCGGCGAGCGCTGGGGTGGGCCC
GGGCAACTACAGCTTCTCCTACCAGCTCGAGGATGAGCCATGGAAGCTGTGTGCGCC
15 TGCACCAGGCTCCACGGCTCGTGGTGCGGTGCGCTTCTGGTGTTCGCTGCCTACA
GCCGACACGTCGAGCTTCGTGCCCCTAGAGTTGCGCGTCACAGCAGCCTCCGGCGC
TCCGCGATATCACCGTGTATCCACATCAATGAAGTAGTGCTCCTAGACGCCCCCG
TGGGGCTGGTGGCGCGGTTGGCTGACGAGAGCGGCCACGTAGTGTTGCGCTGGCTC
CCGCCGCCTGAGACACCCATGACGTCTCACATCCGCTACGAGGTGGACGTCTCGGC
20 CGGCAACGGCGCAGGGAGCGTACAGAGGGTGGAGATCCTGGAGGGCCGCACCGAGT
GTGTGCTGAGCAACCTGCGGGGCGGACGCGCTACACCTTCGCCGTCCGCGCGCGT
ATGGCTGAGCCGAGCTTCGGCGGCTTCTGGAGCGCCTGGTCCGAGCCTGTGTGCGCT
GCTGACGCCTAGCGACCTGGACCCC-3'

Interleukin 4 Receptor25 Sense primerSEQ ID NO: 10

5' -GATCGGATCCATGGGGTGGCTTTGCTCTGGGCTC-3'

Antisense primerSEQ ID NO: 11

30 5' -AGCTTCGAGCGGCCGCGTGCTGCTCGAAGGGCTCCCTGTA-3'

IL-4 Receptor DNA sequence amplifiedSEQ ID NO: 12

5' -ATGGGGTGGCTTTGCTCTGGGCTCCTGTTCCCTGTGAGCTGCCTGGTCCTGCT
GCAGGTGGCAAGCTCTGGGAACATGAAGGTCTTGCAGGAGCCCACCTGCGTCTCCG
5 ACTACATGAGCATCTCTACTTGCGAGTGGAAGATGAATGGTCCCACCAATTGCAGC
ACCGAGCTCCGCCTGTTGTACCAGCTGGTTTTTCTGCTCTCCGAAGCCCACACGTG
TATCCCTGAGAACAACGGAGGCGGGGTGCGTGTGCCACCTGCTCATGGATGACG
TGGTCAGTGCGGATAACTATACACTGGACCTGTGGGCTGGGCAGCAGCTGCTGTGG
AAGGGCTCCTTCAAGCCCAGCGAGCATGTGAAACCCAGGGCCCCAGGAAACCTGAC
10 AGTTCACACCAATGTCTCCGACACTCTGCTGCTGACCTGGAGCAACCCGTATCCCC
CTGACAATTACCTGTATAATCATCTCACCTATGCAGTCAACATTTGGAGTGAAAC
GACCCGGCAGATTTTCAGAATCTATAACGTGACCTACCTAGAACCCTCCCTCCGCAT
CGCAGCCAGCACCCCTGAAGTCTGGGATTTCTACAGGGCACGGGTGAGGGCCTGGG
CTCAGTGCTATAACACCACCTGGAGTGAGTGGAGCCCCAGCACCAAGTGGCACAAAC
15 TCCTACAGGGAGCCCTTCGAGCAGCAC-3'

Interleukin 6 ReceptorSense primerSEQ ID NO: 13

5' -GATCGAATTCATGCTGGCCGTCGGCTGCGCGCTG-3'

20 Antisense primerSEQ ID NO: 14

5' -AGCTTCGAGCGGCCGCATCTTGCACTGGGAGGCTTGTCGC-3'

IL-6 Receptor DNA sequence amplifiedSEQ ID NO: 15

25 ATGCTGGCCGTCGGCTGCGCGCTGCTGGCTGCCCTGCTGGCCGCGCCGGGAGCGGC
GCTGGCCCCAAGGCGCTGCCCTGCGCAGGAGGTGGCAAGAGGCGTGCTGACCAGTC
TGCCAGGAGACAGCGTGACTCTGACCTGCCCCGGGGTAGAGCCGGAAGACAATGCC
ACTGTTCACTGGGTGCTCAGGAAGCCGGCTGCAGGCTCCCACCCCAGCAGATGGGC
TGGCATGGGAAGGAGGCTGCTGCTGAGGTGCGGTGCAGCTCCACGACTCTGGAACT
30 ATTCATGCTACCGGGCCGGCCGCCAGCTGGGACTGTGCACTTGCTGGTGGATGTT
CCCCCGAGGAGCCCCAGCTCTCCTGCTTCCGGAAGAGCCCCCTCAGCAATGTTGT
TTGTGAGTGGGGTCCCTCGGAGCACCCCATCCCTGACGACAAAGGCTGTGCTCTTGG
TGAGGAAGTTTCAGAACAGTCCGGCCGAAGACTTCCAGGAGCCGTGCCAGTATTCC
CAGGAGTCCCAGAAGTTCTCCTGCCAGTTAGCAGTCCCGGAGGGAGACAGCTCTTT

40

CTACATAGTGTCCATGTGCGTCGCCAGTAGTGTGCGGAGCAAGTTCAGCAAACTC
AAACCTTTTCAGGGTTGTGGAATCTTGACGCTGATCCGCTGCCAACATCACAGTC
ACTGCCGTGGCCAGAAACCCCCGCTGGCTCAGTGTACCTGGCAAGACCCCCACTC
CTGGAACATCATCTTTCTACAGACTACGGTTTGAGCTCAGATATCGGGCTGAACGGT
5 CAAAGACATTACAAACATGGATGGTCAAGGACCTCCAGCATCACTGTGTCATCCAC
GACGCCTGGAGCGGCCTGAGGCACGTGGTGCAGCTTCGTGCCCAGGAGGAGTTCGG
GCAAGGCGAGTGGAGCGAGTGGAGCCCGAGGCCATGGGCACGCCTTGACAGAAT
CCAGGAGTCCTCCAGCTGAGAACGAGGTGTCCACCCCATGCAGGCACTTACTACT
AATAAAGACGATGATAATATTCTTCTCAGAGATTCTGCAAATGCGACAAGCCTCCC
10 AGTGCAAGAT-3'

FASSense primerSEQ ID NO: 16

5'-GATCGGATCCATGCTGGGCATCTGGACCCTCCTACC-3'

15 Antisense primerSEQ ID NO: 17

5'-AGCTTCGAGCGGCCGCGTTAGATCTGGATCCTTCCTCTTTGC-3'

FAS DNA sequence amplifiedSEQ ID NO: 18

20 ATGCTGGGCATCTGGACCCTCCTACCTCTGGTTCTTACGTCTGTTGCTAGATTATC
GTCCAAAAGTGTTAATGCCCAAGTGACTGACATCAACTCCAAGGGATTGGAATTGA
GGAAGACTGTTACTACAGTTGAGACTCAGAACTTGAAGGCCTGCATCATGATGGC
CAATTCTGCCATAAGCCCTGTCTCCTCCAGGTGAAAGGAAAGCTAGGGACTGCACAGT
CAATGGGGATGAACCAGACTGCGTGCCCTGCCAAGAAGGGAAGGAGTACACAGACA
25 AAGCCCATTTTTCTTCCAAATGCAGAAGATGTAGATTGTGTGATGAAGGACATGGC
TTAGAAGTGGAATAAACTGCACCCGGACCCAGAATACCAAGTGCAGATGTAAACC
AACTTTTTTTGTAACTCTACTGTATGTGAACACTGTGACCCTTGACCAAATGTG
AACATGGAATCATCAAGGAATGCACACTCACCAGCAACACCAAGTGCAAAGAGGAA
GGATCCAGATCTAAC-3'

30 The amplified DNA fragments and pDNA3-IgG1 vector were both digested with BamH1 and Not I gel purified, as above, and then the amplified fragments ligated into the restriction-digested vector at a position immediately to

the 5' side of the coding region for the hinge-IgG portion of the chimeric protein, again as described above. The recombinant vectors were then used to transfect COS-7 cells, as described above. In each case, the chimeric protein was secreted into the extracellular medium and the ability of each bind its intended ligand was verified.

Example 6: Structure of Secreted Chimeric Protein

Aliquots of the extracellular medium of individual chimeric proteins were electrophoresed on reducing and non-reducing SDS-PAGE gels, along with molecular weight standards and an anti GM-CSF monoclonal antibody (bivalent) control. The antibody control and the chimeric proteins showed a marked increase in electrophoretic mobility on the reducing gel as compared to the non-reducing gel, indicating that the secreted chimeric proteins, like the antibody, are produced as disulfide-linked bivalent dimers.

The foregoing examples illustrate particularly preferred embodiments of the present invention, which is not to be construed as limited thereby. Further embodiments are contained throughout the specification and in the claims which follow. Applicant intends that the scope of the invention be determined from the embodiments described or suggested by the specification as a whole, and equivalents thereof.

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Spinella, Dominic G.
Becherer, Kathleen A.
5 Brown, Steven J.
- (ii) TITLE OF THE INVENTION: COMPOSITIONS AND
METHODS FOR SCREENING DRUG LIBRARIES
- (iii) NUMBER OF SEQUENCES: 19
- (iv) CORRESPONDENCE ADDRESS:
10 (A) ADDRESSEE: Gen-Probe Incorporated
(B) STREET: 9880 Campus Point Drive
(C) CITY: San Diego
(D) STATE: CA
(E) COUNTRY: USA
15 (F) ZIP: 92121
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
20 (D) SOFTWARE: FastSEQ Version 1.5
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:
- 25 (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:

43

- (A) NAME: Fisher, Carlos A
- (B) REGISTRATION NUMBER: 36,510
- (C) REFERENCE/DOCKET NUMBER: CBI016

(ix) TELECOMMUNICATION INFORMATION:

- 5 (A) TELEPHONE: 619-535-2807
- (B) TELEFAX: 619-546-7929
- (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

15 AGCTTCGAGC GGCCGCCGTG CCCAGGGATT GTGGTTGTAA G 41

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GATCCTCGAG TCATTACCA GGAGAGTGGG AGAGGCT 37

(2) INFORMATION FOR SEQ ID NO:3:

- 25 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 34 base pairs

44

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

5 GATCGGATCC ATGGGCCTCT CCACCGTGCC TGAC

34

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- 10 (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

AGCTTCGAGC GGCCGCTGTG GTGCCTGAGT CCTCAGTGCC

40

(2) INFORMATION FOR SEQ ID NO:5:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6338 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GACGGATCGG	GAGATCTCCC	GATCCCCTAT	GGTCGACTCT	40
CAGTACAATC	TGCTCTGATG	CCGCATAGTT	AAGCCAGTAT	80
CTGCTCCCTG	CTTGTGTGTT	GGAGGTCGCT	GAGTAGTGCG	120
CGAGCAAAAT	TTAAGCTACA	ACAAGGCAAG	GCTTGACCGA	160
25 CAATTGCATG	AAGAATCTGC	TTAGGGTTAG	GCGTTTTGCG	200
CTGCTTCGCG	ATGTACGGGC	CAGATATACG	CGTTGACATT	240
GATTATTGAC	TAGTTATTAA	TAGTAATCAA	TTACGGGGTC	280

	ATTAGTTCAT	AGCCCATATA	TGGAGTTCCG	CGTTACATAA	320
	CTTACGGTAA	ATGGCCCCGCC	TGGCTGACCG	CCCAACGACC	360
	CCCGCCCCATT	GACGTCAATA	ATGACGTATG	TTCCCATAGT	400
	AACGCCAATA	GGGACTTTCC	ATTGACGTCA	ATGGGTGGAC	440
5	TATTTACGGT	AAACTGCCCA	CTTGGCAGTA	CATCAAGTGT	480
	ATCATATGCC	AAGTACGCCC	CCTATTGACG	TCAATGACGG	520
	TAAATGGCCC	GCCTGGCATT	ATGCCCAGTA	CATGACCTTA	560
	TGGGACTTTC	CTACTTGGCA	GTACATCTAC	GTATTAGTCA	600
	TCGCTATTAC	CATGGTGATG	CGGTTTTGGC	AGTACATCAA	640
10	TGGGCGTGGA	TAGCGGTTTG	ACTCACGGGG	ATTTCCAAGT	680
	CTCCACCCCA	TTGACGTCAA	TGGGAGTTTG	TTTTGGCACC	720
	AAAATCAACG	GGACTTTCCA	AAATGTCGTA	ACAACTCCGC	760
	CCCATTGACG	CAAATGGGCG	GTAGGCGTGT	ACGGTGGGAG	800
	GTCTATATAA	GCAGAGCTCT	CTGGCTAACT	AGAGAACCCA	840
15	CTGCTTACTG	GCTTATCGAA	ATTAATACGA	CTCACTATAG	880
	GGAGACCCAA	GCTGGCTAGC	GTTTAAACTT	AAGCTTGGTA	920
	CCGAGCTCGG	ATCCACTAGT	CCAGTGTGGT	GGAATTCTGC	960
	AGATATCCAG	CACAGTGGCG	GCCGCCGTGC	CCAGGGATTG	1000
	TGGTTGTAAG	CCTTGCAAT	GTACAGGTAA	GTCAGTGGCC	1040
20	TTCACCTGAC	CCAGATGCAA	CAAGTGGCAA	TGGTTGGAGG	1080
	GTGGCCAGGT	ATTGACCTAT	TTCCACCTTT	CTTCTTCATC	1120
	CTTAGTCCCA	GAAGTATCAT	CTGTCTTCAT	CTTCCCCCCA	1160
	AAGCCCAAGG	ATGTGCTCAC	CATTACTCTG	ACTCCTAAGG	1200
	TCACGTGTGT	TGTGGTAGAC	ATCAGCAAGG	ATGATCCCGA	1240
25	GGTCCAGTTC	AGCTGGTTTG	TAGATGATGT	GGAGGTGCAC	1280
	ACAGCTCAGA	CGCAACCCCG	GGAGGAGCAG	TTCAACAGCA	1320
	CTTTCCGCTC	AGTCAGTGAA	CTTCCCATCA	TGCACCAGGA	1360
	CTGGCTCAAT	GGCAAGGAGT	TCAAATGCAG	GGTCAACAGT	1400
	GCAGCTTTCC	CTGCCCCCAT	CGAGAAAACC	ATCTCCAAAA	1440
30	CCAAAGGTGA	GAGCTGCAGT	GTGTGACATA	GAAGCTGCAA	1480
	TAGTCAGTCC	ATAGACAGAG	CTTGGCATAA	CAGACCCCTG	1520
	CCCTGTTTCGT	GACCTCTGTG	CTGACCAATC	TCTTTACCCA	1560
	CCCACAGGCA	GACCGAAGGC	TCCACAGGTG	TACACCATTC	1600
	CACCTCCCAA	GGAGCAGATG	GCCAAGGATA	AAGTCAGTCT	1640
35	GACCGCCATG	ATAACAGACT	TCTTCCCTGA	AGACATTACT	1680
	GTGGAGTGGC	AGTGGAATGG	GCAGCCAGCG	GAGAACTACA	1720
	AGAACACTCA	GCCCATCATG	AACACGAATG	GCTCTTACTT	1760

	CGTCTACAGC	AAGCTCAATG	TGCAGAAGAG	CAACTGGGAG	1800
	GCAGGAAATA	CTTTCACCTG	CTCTGTGTTA	CATGAGGGCC	1840
	TACACAACCA	CCATACTGAG	AAGAGCCTCT	CCCACTCTCC	1880
	TGGTAAATGA	CTCGAGTCTA	GAGGGCCCCG	TTAAACCCGC	1920
5	TGATCAGCCT	CGACTGTGCC	TTCTAGTTGC	CAGCCATCTG	1960
	TTGTTTGCCC	CTCCCCCGTG	CCTTCCTTGA	CCCTGGAAGG	2000
	TGCCACTCCC	ACTGTCCTTT	CCTAATAAAA	TGAGGAAATT	2040
	GCATCGCATT	GTCTGAGTAG	GTGTCATTCT	ATTCTGGGGG	2080
	GTGGGGTGGG	GCAGGACAGC	AAGGGGGAGG	ATTGGGAAGA	2120
10	CAATAGCAGG	CATGCTGGGG	ATGCGGTGGG	CTCTATGGCT	2160
	TCTGAGGCGG	AAAGAACCAG	CTGGGGCTCT	AGGGGGTATC	2200
	CCCACGCGCC	CTGTAGCGGC	GCATTAAGCG	CGGCGGGTGT	2240
	GGTGGTTACG	CGCAGCGTGA	CCGCTACACT	TGCCAGCGCC	2280
	CTAGCGCCCC	CTCCTTTTCG	TTTCTTCCCT	TCCTTTCTCG	2320
15	CCACGTTTCG	CGGCTTTCCC	CGTCAAGCTC	TAAATCGGGG	2360
	CATCCCTTTA	GGGTTCGGAT	TTAGTGCTTT	ACGGCACCTC	2400
	GACCCCAAAA	AACTTGATTA	GGGTGATGGT	TCACGTAGTG	2440
	GGCCATCGCC	CTGATAGACG	GTTTTTCGCC	CTTTGACGTT	2480
	GGAGTCCACG	TTCTTTAATA	GTGGACTCTT	GTTCCAAACT	2520
20	GGAACAACAC	TCAACCCTAT	CTCGGTCTAT	TCTTTTGATT	2560
	TATAAGGGAT	TTTGGGGATT	TCGGCCTATT	GGTTAAAAAA	2600
	TGAGCTGATT	TAACAAAAAT	TTAACGCGAA	TTAATTCTGT	2640
	GGAATGTGTG	TCAGTTAGGG	TGTGGAAAGT	CCCCAGGCTC	2680
	CCCAGGCAGG	CAGAAGTATG	CAAAGCATGC	ATCTCAATTA	2720
25	GTCAGCAACC	AGGTGTGGAA	AGTCCCCAGG	CTCCCCAGCA	2760
	GGCAGAAGTA	TGCAAAGCAT	GCATCTCAAT	TAGTCAGCAA	2800
	CCATAGTCCC	GCCCCTAACT	CCGCCCATCC	CGCCCCTAAC	2840
	TCCGCCCAGT	TCCGCCCATT	CTCCGCCCCA	TGGCTGACTA	2880
	ATTTTTTTTA	TTTATGCAGA	GGCCGAGGCC	GCCTCTGCCT	2920
30	CTGAGCTATT	CCAGAAGTAG	TGAGGAGGCT	TTTTTGGAGG	2960
	CCTAGGCTTT	TGCAAAAAGC	TCCCGGGAGC	TTGTATATCC	3000
	ATTTTCGGAT	CTGATCAAGA	GACAGGATGA	GGATCGTTTC	3040
	GCATGATTGA	ACAAGATGGA	TTGCACGCAG	GTTCTCCGGC	3080
	CGCTTGGGTG	GAGAGGCTAT	TCGGCTATGA	CTGGGCACAA	3120
35	CAGACAATCG	GCTGCTCTGA	TGCCGCCGTG	TTCCGGCTGT	3160
	CAGCGCAGGG	GCGCCCGGTT	CTTTTGTGCA	AGACCGACCT	3200
	GTCCGGTGCC	CTGAATGAAC	TGCAGGACGA	GGCAGCGCGG	3240

	CTATCGTGGC	TGGCCACGAC	GGGCGTTCCT	TGCGCAGCTG	3280
	TGCTCGACGT	TGTCACTGAA	GCGGGAAGGG	ACTGGCTGCT	3320
	ATTGGGCGAA	GTGCCGGGGC	AGGATCTCCT	GTCATCTCAC	3360
	CTTGCTCCTG	CCGAGAAAAGT	ATCCATCATG	GCTGATGCAA	3400
5	TGCGGCGGCT	GCATACGCTT	GATCCGGCTA	CCTGCCCATT	3440
	CGACCACCAA	GCGAAACATC	GCATCGAGCG	AGCACGTACT	3480
	CGGATGGAAG	CCGGTCTTGT	CGATCAGGAT	GATCTGGACG	3520
	AAGAGCATCA	GGGGCTCGCG	CCAGCCGAAC	TGTTCCGCCAG	3560
	GCTCAAGGCG	CGCATGCCCG	ACGGCGAGGA	TCTCGTCGTG	3600
10	ACCCATGGCG	ATGCCTGCTT	GCCGAATATC	ATGGTGGAAA	3640
	ATGGCCGCTT	TTCTGGATTG	ATCGACTGTG	GCCGGCTGGG	3680
	TGTGGCGGAC	CGCTATCAGG	ACATAGCGTT	GGCTACCCGT	3720
	GATATTGCTG	AAGAGCTTGG	CGGCGAATGG	GCTGACCGCT	3760
	TCCTCGTGCT	TTACGGTATC	GCCGCTCCCG	ATTCGCAGCG	3800
15	CATCGCCTTC	TATCGCCTTC	TTGACGAGTT	CTTCTGAGCG	3840
	GGACTCTGGG	GTTCGAAATG	ACCGACCAAG	CGACGCCCAA	3880
	CCTGCCATCA	CGAGATTTTC	ATTCCACCGC	CGCCTTCTAT	3920
	GAAAGGTTGG	GCTTCGGAAT	CGTTTTCCGG	GACGCCGGCT	3960
	GGATGATCCT	CCAGCGCGGG	GATCTCATGC	TGGAGTTCTT	4000
20	CGCCCACCCC	AACTTGTTTA	TTGCAGCTTA	TAATGGTTAC	4040
	AAATAAAGCA	ATAGCATCAC	AAATTTTACA	AATAAAGCAT	4080
	TTTTTTTCACT	GCATTCTAGT	TGTGGTTTGT	CCAAACTCAT	4120
	CAATGTATCT	TATCATGTCT	GTATACCGTC	GACCTCTAGC	4160
	TAGAGCTTGG	CGTAATCATG	GTCATAGCTG	TTTCCTGTGT	4200
25	GAAATTGTTA	TCCGCTCACA	ATTCCACACA	ACATACGAGC	4240
	CGGAAGCATA	AAGTGTAAG	CCTGGGGTGC	CTAATGAGTG	4280
	AGCTAACTCA	CATTAATTGC	GTTGCGCTCA	CTGCCCCTT	4320
	TCCAGTCGGG	AAACCTGTCT	TGCCAGCTGC	ATTAATGAAT	4360
	CGGCCAACGC	GCGGGGAGAG	GCGGTTTGCG	TATTGGGCGC	4400
30	TCTTCCGCTT	CCTCGCTCAC	TGACTCGCTG	CGCTCGGTCTG	4440
	TTCCGGCTGCG	GCGAGCGGTA	TCAGCTCACT	CAAAGGCGGT	4480
	AATACGGTTA	TCCACAGAAT	CAGGGGATAA	CGCAGGAAAG	4520
	AACATGTGAG	CAAAAGGCCA	GCAAAAGGCC	AGGAACCGTA	4560
	AAAAGGCCGC	GTTGCTGGCG	TTTTTCCATA	GGCTCCGCCC	4600
35	CCCTGACGAG	CATCACAAAA	ATCGACGCTC	AAGTCAGAGG	4640
	TGGCGAAACC	CGACAGGACT	ATAAAGATAC	CAGGCGTTTC	4680
	CCCCTGGAAG	CTCCCTCGTG	CGCTCTCCTG	TTCCGACCCT	4720

	GCCGCTTACC	GGATACCTGT	CCGCCTTTCT	CCCTTCGGGA	4760
	AGCGTGCGC	TTTCTCAATG	CTCACGCTGT	AGGTATCTCA	4800
	GTTCCGGTGA	GGTCGTTTCG	TCCAAGCTGG	GCTGTGTGCA	4840
	CGAACCCCCC	G TTCAGCCCC	ACCGCTGCGC	CTTATCCGGT	4880
5	AACTATCGTC	TTGAGTCCAA	CCCGGTAAGA	CACGACTTAT	4920
	CGCCACTGGC	AGCAGCCACT	GGTAACAGGA	TTAGCAGAGC	4960
	GAGGTATGTA	GGCGGTGCTA	CAGAGTTCTT	GAAGTGGTGG	5000
	CCTAACTACG	GCTACACTAG	AAGGACAGTA	TTTGGTATCT	5040
	GCGCTCTGCT	GAAGCCAGTT	ACCTTCGGAA	AAAGAGTTGG	5080
10	TAGCTCTTGA	TCCGGCAAAC	AAACCACCGC	TGGTAGCGGT	5120
	GGTTTTTTTT	TTTGCAAGCA	GCAGATTACG	CGCAGAAAAA	5160
	AAGGATCTCA	AGAAGATCCT	TTGATCTTTT	CTACGGGGTC	5200
	TGACGCTCAG	TGGAACGAAA	ACTCACGTTA	AGGGATTTTG	5240
	GTCATGAGAT	TATCAAAAAG	GATCTTCACC	TAGATCCTTT	5280
15	TAAATTAAAA	ATGAAGTTTT	AAATCAATCT	AAAGTATATA	5320
	TGAGTAAACT	TGGTCTGACA	GTTACCAATG	CTTAATCAGT	5360
	GAGGCACCTA	TCTCAGCGAT	CTGTCTATTT	CGTTCATCCA	5400
	TAGTTGCCTG	ACTCCCCGTC	GTGTAGATAA	CTACGATACG	5440
	GGAGGGCTTA	CCATCTGGCC	CCAGTGCTGC	AATGATACCG	5480
20	CGAGACCCAC	GCTCACC GGC	TCCAGATTTA	TCAGCAATAA	5520
	ACCAGCCAGC	CGGAAGGGCC	GAGCGCAGAA	GTGGTCCTGC	5560
	AACTTTATCC	GCCTCCATCC	AGTCTATTAA	TTGTTGCCGG	5600
	GAAGCTAGAG	TAAGTAGTTC	GCCAGTTAAT	AGTTTGCGCA	5640
	ACGTTGTTGC	CATTGCTACA	GGCATCGTGG	TGTCACGCTC	5680
25	GTCGTTTGGT	ATGGCTTCAT	TCAGCTCCGG	TTCCCAACGA	5720
	TCAAGGCGAG	TTACATGATC	CCCCATGTTG	TGCAAAAAAG	5760
	CGGTTAGCTC	CTTCGGTCCT	CCGATCGTTG	TCAGAAGTAA	5800
	GTTGGCCGCA	GTGTTATCAC	TCATGGTTAT	GGCAGCACTG	5840
	CATAATTCTC	TTACTGT CAT	GCCATCCGTA	AGATGCTTTT	5880
30	CTGTGACTGG	TGAGTACTCA	ACCAAGTCAT	TCTGAGAATA	5920
	GTGTATGCGG	CGACCGAGTT	GCTCTTGCCC	GGCGTCAATA	5960
	CGGGATAATA	CCGCGCCACA	TAGCAGAACT	TTAAAAGTGC	6000
	TCATCATTGG	AAAACGTTCT	TCGGGGCGAA	AACTCTCAAG	6040
	GATCTTACCG	CTGTTGAGAT	CCAGTTCGAT	GTAACCCACT	6080
35	CGTGCACCCA	ACTGATCTTC	AGCATCTTTT	ACTTTCACCA	6120
	GCGTTTCTGG	GTGAGCAAAA	ACAGGAAGGC	AAAATGCCGC	6160
	AAAAAAGGGA	ATAAGGGCGA	CACGGAAATG	TTGAATACTC	6200

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ATACTCTTCC	TTTTTCAATA	TTATTGAAGC	ATTTATCAGG	6240
GTTATTGTCT	CATGAGCGGA	TACATATTTG	AATGTATTTA	6280
GAAAAATAAA	CAAATAGGGG	TTCCGCGCAC	ATTTCCCCGA	6320
AAAGTGCCAC	CTGACGTC			6338

5 (2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6926 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- 10 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

	GACGGATCGG	GAGATCTCCC	GATCCCCTAT	GGTCGACTCT	40
	CAGTACAATC	TGCTCTGATG	CCGCATAGTT	AAGCCAGTAT	80
	CTGCTCCCTG	CTTGTGTGTT	GGAGGTCGCT	GAGTAGTGCG	120
15	CGAGCAAAAT	TTAAGCTACA	ACAAGGCAAG	GCTTGACCGA	160
	CAATTGCATG	AAGAATCTGC	TTAGGGTTAG	GCGTTTTGCG	200
	CTGCTTCGCG	ATGTACGGGC	CAGATATACG	CGTTGACATT	240
	GATTATTGAC	TAGTTATTAA	TAGTAATCAA	TTACGGGGTC	280
	ATTAGTTCAT	AGCCCATATA	TGGAGTTCCG	CGTTACATAA	320
20	CTTACGGTAA	ATGGCCCGCC	TGGCTGACCG	CCCAACGACC	360
	CCCGCCCAT	GACGTCAATA	ATGACGTATG	TTCCCATAGT	400
	AACGCCAATA	GGGACTTTCC	ATTGACGTCA	ATGGGTGGAC	440
	TATTTACGGT	AAACTGCCCA	CTTGGCAGTA	CATCAAGTGT	480
	ATCATATGCC	AAGTACGCCC	CCTATTGACG	TCAATGACGG	520
25	TAAATGGCCC	GCCTGGCATT	ATGCCCAGTA	CATGACCTTA	560
	TGGGACTTTC	CTACTTGGCA	GTACATCTAC	GTATTAGTCA	600
	TCGCTATTAC	CATGGTGATG	CGGTTTTGGC	AGTACATCAA	640
	TGGGCGTGGA	TAGCGGTTTG	ACTCACGGGG	ATTTCCAAGT	680
	CTCCACCCCA	TTGACGTCAA	TGGGAGTTTG	TTTTGGCACC	720
30	AAAATCAACG	GGAATTTCCA	AAATGTCGTA	ACAATCCGC	760
	CCCATTGACG	CAAATGGGCG	GTAGGCGTGT	ACGGTGGGAG	800
	GTCTATATAA	GCAGAGCTCT	CTGGCTAACT	AGAGAACCCA	840
	CTGCTTACTG	GCTTATCGAA	ATTAATACGA	CTCACTATAG	880

	GGAGACCCAA	GCTGGCTAGC	GTTTAAACTT	AAGCTTGGTA	920
	CCGAGCTCGG	ATCCATGGGC	CTCTCCACCG	TGCCTGACCT	960
	GCTGCTGCCG	CTGGTGCTCC	TGGAGCTGTT	GGTGGGAATA	1000
	TACCCCTCAG	GGGTATTGG	ACTGGTCCCT	CACCTAGGGG	1040
5	ACAGGGAGAA	GAGAGATAGT	GTGTGTCCCC	AAGGAAAATA	1080
	TATCCACCCT	CAAAATAATT	CGATTTGCTG	TACCAAGTGC	1120
	CACAAAGGAA	CCTACTTGTA	CAATGACTGT	CCAGGCCCCG	1160
	GGCAGGATAC	GGACTGCAGG	GAGTGTGAGA	GCGGCTCCTT	1200
	CACCGCTTCA	GAAAACCACC	TCAGACACTG	CCTCAGCTGC	1240
10	TCCAAATGCC	GAAAGGAAAT	GGGTCAGGTG	GAGATCTCTT	1280
	CTTGACAGT	GGACCGGGAC	ACCGTGTGTG	GCTGCAGGAA	1320
	GAACCAGTAC	CGGCATTATT	GGAGTGAAAA	CCTTTTCCAG	1360
	TGCTTCAATT	GCAGCCTCTG	CCTCAATGGG	ACCGTGCACC	1400
	TCTCCTGCCA	GGAGAAACAG	AACACCGTGT	GCACCTGCCA	1440
15	TGCAGGTTTC	TTTCTAAGAG	AAAACGAGTG	TGTCTCCTGT	1480
	AGTAACTGTA	AGAAAAGCCT	GGAGTGCACG	AAGTTGTGCC	1520
	TACCCAGAT	TGAGAATGTT	AAGGGCACTG	AGGACTCAGG	1560
	CACCACAGCG	GCCGCCGTGC	CCAGGGATTG	TGGTTGTAAG	1600
	CCTTGACATAT	GTACAGGTAA	GTCAGTGGCC	TTCACCTGAC	1640
20	CCAGATGCAA	CAAGTGGA	TGGTTGGAGG	GTGGCCAGGT	1680
	ATTGACCTAT	TTCCACCTTT	CTTCTTCATC	CTTAGTCCCA	1720
	GAAGTATCAT	CTGTCTTCAT	CTTCCCCCA	AAGCCCAAGG	1760
	ATGTGCTCAC	CATTACTCTG	ACTCCTAAGG	TCACGTGTGT	1800
	TGTGGTAGAC	ATCAGCAAGG	ATGATCCCGA	GGTCCAGTTC	1840
25	AGCTGGTTTG	TAGATGATGT	GGAGGTGCAC	ACAGCTCAGA	1880
	CGCAACCCCG	GGAGGAGCAG	TTCAACAGCA	CTTTCCGCTC	1920
	AGTCAGTGAA	CTTCCCATCA	TGCACCAGGA	CTGGCTCAAT	1960
	GGCAAGGAGT	TCAAATGCAG	GGTCAACAGT	GCAGCTTTCC	2000
	CTGCCCCCAT	CGAGAAAACC	ATCTCCAAAA	CCAAAGGTGA	2040
30	GAGCTGCAGT	GTGTGACATA	GAAGCTGCAA	TAGTCAGTCC	2080
	ATAGACAGAG	CTTGGCATAA	CAGACCCCTG	CCCTGTTCGT	2120
	GACCTCTGTG	CTGACCAATC	TCTTTACCCA	CCCACAGGCA	2160
	GACCGAAGGC	TCCACAGGTG	TACACCATTC	CACCTCCCAA	2200
	GGAGCAGATG	GCCAAGGATA	AAGTCAGTCT	GACCGCCATG	2240
35	ATAACAGACT	TCTTCCCTGA	AGACATTACT	GTGGAGTGGC	2280
	AGTGGAATGG	GCAGCCAGCG	GAGAACTACA	AGAACACTCA	2320
	GCCCATCATG	AACACGAATG	GCTCTTACTT	CGTCTACAGC	2360

	AAGCTCAATG	TGCAGAAAGAG	CAACTGGGAG	GCAGGAAATA	2400
	CTTTCACCTG	CTCTGTGTTA	CATGAGGGCC	TACACAACCA	2440
	CCATACTGAG	AAGAGCCTCT	CCCACTCTCC	TGGTAAATGA	2480
	CTCGAGTCTA	GAGGGCCCGT	TTAAACCCGC	TGATCAGCCT	2520
5	CGACTGTGCC	TTCTAGTTGC	CAGCCATCTG	TTGTTTGCCC	2560
	CTCCCCCGTG	CCTTCCTTGA	CCCTGGAAGG	TGCCACTCCC	2600
	ACTGTCCTTT	CCTAATAAAA	TGAGGAAATT	GCATCGCATT	2640
	GTCTGAGTAG	GTGTCATTCT	ATTCTGGGGG	GTGGGGTGGG	2680
	GCAGGACAGC	AAGGGGGAGG	ATTGGGAAGA	CAATAGCAGG	2720
10	CATGCTGGGG	ATGCGGTGGG	CTCTATGGCT	TCTGAGGCGG	2760
	AAAGAACCAG	CTGGGGCTCT	AGGGGGTATC	CCCACGCGCC	2800
	CTGTAGCGGC	GCATTAAGCG	CGGCGGGTGT	GGTGGTTACG	2840
	CGCAGCGTGA	CCGCTACACT	TGCCAGCGCC	CTAGCGCCCCG	2880
	CTCCTTTTCGC	TTTCTTCCCT	TCCTTTCTCG	CCACGTTTCGC	2920
15	CGGCTTTCCC	CGTCAAGCTC	TAAATCGGGG	CATCCCTTTA	2960
	GGGTTCCGAT	TTAGTGCTTT	ACGGCACCTC	GACCCCAAAA	3000
	AACTTGATTA	GGGTGATGGT	TCACGTAGTG	GGCCATCGCC	3040
	CTGATAGACG	GTTTTTCGCC	CTTTGACGTT	GGAGTCCACG	3080
	TTCTTTAATA	GTGGACTCTT	GTTCCAAACT	GGAACAACAC	3120
20	TCAACCCTAT	CTCGGTCTAT	TCTTTTGATT	TATAAGGGAT	3160
	TTTGGGGATT	TCGGCCTATT	GGTTAAAAAA	TGAGCTGATT	3200
	TAACAAAAAT	TTAACGCGAA	TTAATTCTGT	GGAATGTGTG	3240
	TCAGTTAGGG	TGTGGAAAGT	CCCCAGGCTC	CCCAGGCAGG	3280
	CAGAAGTATG	CAAAGCATGC	ATCTCAATTA	GTCAGCAACC	3320
25	AGGTGTGGAA	AGTCCCCAGG	CTCCCCAGCA	GGCAGAAGTA	3360
	TGCAAAGCAT	GCATCTCAAT	TAGTCAGCAA	CCATAGTCCC	3400
	GCCCCTAACT	CCGCCCATCC	CGCCCCTAAC	TCCGCCCAGT	3440
	TCCGCCCAT	CTCCGCCCCA	TGGCTGACTA	ATTTTTTTTA	3480
	TTTATGCAGA	GGCCGAGGCC	GCCTCTGCCT	CTGAGCTATT	3520
30	CCAGAAGTAG	TGAGGAGGCT	TTTTTGGAGG	CCTAGGCTTT	3560
	TGCAAAAAGC	TCCCGGGAGC	TTGTATATCC	ATTTTCGGAT	3600
	CTGATCAAGA	GACAGGATGA	GGATCGTTTC	GCATGATTGA	3640
	ACAAGATGGA	TTGCACGCAG	GTTCTCCGGC	CGCTTGGGTG	3680
	GAGAGGCTAT	TCGGCTATGA	CTGGGCACAA	CAGACAATCG	3720
35	GCTGCTCTGA	TGCCGCCGTG	TTCCGGCTGT	CAGCGCAGGG	3760
	GCGCCCGGTT	CTTTTTGTCA	AGACCGACCT	GTCCGGTGCC	3800
	CTGAATGAAC	TGCAGGACGA	GGCAGCGCGG	CTATCGTGCC	3840

	TGGCCACGAC	GGGCGTTCCT	TGCGCAGCTG	TGCTCGACGT	3880
	TGTCACTGAA	GCGGGAAGGG	ACTGGCTGCT	ATTGGGCGAA	3920
	GTGCCGGGGC	AGGATCTCCT	GTCATCTCAC	CTTGCTCCTG	3960
	CCGAGAAAGT	ATCCATCATG	GCTGATGCAA	TGCGGCGGCT	4000
5	GCATACGCTT	GATCCGGCTA	CCTGCCCCATT	CGACCACCAA	4040
	GCGAAACATC	GCATCGAGCG	AGCACGTACT	CGGATGGAAG	4080
	CCGGTCTTGT	CGATCAGGAT	GATCTGGACG	AAGAGCATCA	4120
	GGGGCTCGCG	CCAGCCGAAC	TGTTCCGCCAG	GCTCAAGGCG	4160
	CGCATGCCCC	ACGGCGAGGA	TCTCGTCGTG	ACCCATGGCG	4200
10	ATGCCTGCTT	GCCGAATATC	ATGGTGGAAG	ATGGCCGCTT	4240
	TTCTGGATTG	ATCGACTGTG	GCCGGCTGGG	TGTGGCGGAC	4280
	CGCTATCAGG	ACATAGCGTT	GGCTACCCGT	GATATTGCTG	4320
	AAGAGCTTGG	CGGCGAATGG	GCTGACCGCT	TCCTCGTGCT	4360
	TTACGGTATC	GCCGCTCCCG	ATTGCGAGCG	CATCGCCTTC	4400
15	TATCGCCTTC	TTGACGAGTT	CTTCTGAGCG	GGACTCTGGG	4440
	GTTCGAAATG	ACCGACCAAG	CGACGCCCAA	CCTGCCATCA	4480
	CGAGATTTTC	ATTCCACCGC	CGCCTTCTAT	GAAAGGTTGG	4520
	GCTTCGGAAT	CGTTTTCCGG	GACGCCGGCT	GGATGATCCT	4560
	CCAGCGCGGG	GATCTCATGC	TGGAGTTCTT	CGCCCACCCC	4600
20	AACTTGTTTA	TTGCAGCTTA	TAATGGTTAC	AAATAAAGCA	4640
	ATAGCATCAC	AAATTTTACA	AATAAAGCAT	TTTTTTTCACT	4680
	GCATTCTAGT	TGTGGTTTGT	CCAAACTCAT	CAATGTATCT	4720
	TATCATGTCT	GTATACCGTC	GACCTCTAGC	TAGAGCTTGG	4760
	CGTAATCATG	GTCATAGCTG	TTTCCTGTGT	GAAATTGTTA	4800
25	TCCGCTCACA	ATTCCACACA	ACATACGAGC	CGGAAGCATA	4840
	AAGTGTAAG	CCTGGGGTGC	CTAATGAGTG	AGCTAACTCA	4880
	CATTAATTGC	GTTGCGCTCA	CTGCCCCGCTT	TCCAGTCGGG	4920
	AAACCTGTCT	TGCCAGCTGC	ATTAATGAAT	CGGCCAACGC	4960
	GCGGGGAGAG	GCGGTTTGCG	TATTGGGCGC	TCTTCCGCTT	5000
30	CCTCGCTCAC	TGACTCGCTG	CGCTCGGTGC	TTCGGCTGCG	5040
	GCGAGCGGTA	TCAGCTCACT	CAAAGGCGGT	AATACGGTTA	5080
	TCCACAGAAT	CAGGGGATAA	CGCAGGAAAG	AACATGTGAG	5120
	CAAAAGGCCA	GCAAAAGGCC	AGGAACCGTA	AAAAGGCCGC	5160
	GTTGCTGGCG	TTTTTCCATA	GGCTCCGCCC	CCCTGACGAG	5200
35	CATCACAAAA	ATCGACGCTC	AAGTCAGAGG	TGGCGAAACC	5240
	CGACAGGACT	ATAAAGATAC	CAGGCGTTTC	CCCCTGGAAG	5280
	CTCCCTCGTG	CGCTCTCCTG	TTCCGACCCT	GCCGCTTACC	5320

	GGATACCTGT	CCGCCTTTCT	CCCTTCGGGA	AGCGTGGCGC	5360
	TTTCTCAATG	CTCACGCTGT	AGGTATCTCA	GTTCGGTGTA	5400
	GGTCGTTCGC	TCCAAGCTGG	GCTGTGTGCA	CGAACCCCCC	5440
	GTTCAGCCCCG	ACCGCTGCGC	CTTATCCGGT	AACTATCGTC	5480
5	TTGAGTCCAA	CCCGGTAAGA	CACGACTTAT	CGCCACTGGC	5520
	AGCAGCCACT	GGTAACAGGA	TTAGCAGAGC	GAGGTATGTA	5560
	GGCGGTGCTA	CAGAGTTCTT	GAAGTGGTGG	CCTAACTACG	5600
	GCTACACTAG	AAGGACAGTA	TTTGGTATCT	GCGCTCTGCT	5640
	GAAGCCAGTT	ACCTTCGGAA	AAAGAGTTGG	TAGCTCTTGA	5680
10	TCCGGCAAAC	AAACCACCGC	TGGTAGCGGT	GGTTTTTTTG	5720
	TTTGCAAGCA	GCAGATTACG	CGCAGAAAAA	AAGGATCTCA	5760
	AGAAGATCCT	TTGATCTTTT	CTACGGGGTC	TGACGCTCAG	5800
	TGGAACGAAA	ACTCACGTTA	AGGGATTTTG	GTCATGAGAT	5840
	TATCAAAAAG	GATCTTCACC	TAGATCCTTT	TAAATTAAAA	5880
15	ATGAAGTTTT	AAATCAATCT	AAAGTATATA	TGAGTAAACT	5920
	TGGTCTGACA	GTTACCAATG	CTTAATCAGT	GAGGCACCTA	5960
	TCTCAGCGAT	CTGTCTATTT	CGTTCATCCA	TAGTTGCCTG	6000
	ACTCCCCGTC	GTGTAGATAA	CTACGATACG	GGAGGGCTTA	6040
	CCATCTGGCC	CCAGTGCTGC	AATGATACCG	CGAGACCCAC	6080
20	GCTCACCGGC	TCCAGATTTA	TCAGCAATAA	ACCAGCCAGC	6120
	CGGAAGGGCC	GAGCGCAGAA	GTGGTCCTGC	AACTTTATCC	6160
	GCCTCCATCC	AGTCTATTAA	TTGTTGCCGG	GAAGCTAGAG	6200
	TAAGTAGTTC	GCCAGTTAAT	AGTTTGCGCA	ACGTTGTTGC	6240
	CATTGCTACA	GGCATCGTGG	TGTCACGCTC	GTCGTTTGGT	6280
25	ATGGCTTCAT	TCAGCTCCGG	TTCCCAACGA	TCAAGGCGAG	6320
	TTACATGATC	CCCCATGTTG	TGCAAAAAAG	CGGTTAGCTC	6360
	CTTCGGTCCT	CCGATCGTTG	TCAGAAGTAA	GTTGGCCGCA	6400
	GTGTTATCAC	TCATGGTTAT	GGCAGCACTG	CATAATTCTC	6440
	TTACTGTCAT	GCCATCCGTA	AGATGCTTTT	CTGTGACTGG	6480
30	TGAGTACTCA	ACCAAGTCAT	TCTGAGAATA	GTGTATGCGG	6520
	CGACCGAGTT	GCTCTTGCCC	GGCGTCAATA	CGGGATAATA	6560
	CCGCGCCACA	TAGCAGAACT	TTAAAAGTGC	TCATCATTGG	6600
	AAAACGTTCT	TCGGGGCGAA	AACTCTCAAG	GATCTTACCG	6640
	CTGTTGAGAT	CCAGTTCGAT	GTAACCCACT	CGTGCACCCA	6680
35	ACTGATCTTC	AGCATCTTTT	ACTTTCACCA	GCGTTTCTGG	6720
	GTGAGCAAAA	ACAGGAAGGC	AAAATGCCGC	AAAAAAGGGA	6760
	ATAAGGGCGA	CACGGAAATG	TTGAATACTC	ATACTCTTCC	6800

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TTTTTCAATA TTATTGAAGC ATTTATCAGG GTTATTGTCT	6840
CATGAGCGGA TACATATTTG AATGTATTTA GAAAAATAAA	6880
CAAATAGGGG TTCCGCGCAC ATTTCCCCGA AAAGTGCCAC	6920
CTGACG	6926

5 (2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- 10 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GATCGGATCC ATGGACCACC TCGGGGCGTC CCTC	34
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(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

20 AGCTTCGAGC GGCCGCGGGG TCCAGGTCGC TAGGCGTCAG	40
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(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 750 base pairs
- (B) TYPE: nucleic acid
- 25 (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

	ATGGACCACC	TCGGGGCGTC	CCTCTGGCCC	CAGGTCGGCT	40
	CCCTTTGTCT	CCTGCTCGCT	GGGGCCGCCT	GGGCGCCCCC	80
	GCCTAACCTC	CCGGACCCCA	AGTTCGAGAG	CAAAGCGGCC	120
5	TTGCTGGCGG	CCCGGGGGCC	CGAAGAGCTT	CTGTGCTTCA	160
	CCGAGCGGTT	GGAGGACTTG	GTGTGTTTCT	GGGAGGAAGC	200
	GGCGAGCGCT	GGGGTGGGCC	CGGGCAACTA	CAGCTTCTCC	240
	TACCAGCTCG	AGGATGAGCC	ATGGAAGCTG	TGTCGCCTGC	280
	ACCAGGCTCC	CACGGCTCGT	GGTGCGGTGC	GCTTCTGGTG	320
10	TTCGCTGCCT	ACAGCCGACA	CGTCGAGCTT	CGTGCCCCTA	360
	GAGTTGCGCG	TCACAGCAGC	CTCCGGCGCT	CCGCGATATC	400
	ACCGTGTCAT	CCACATCAAT	GAAGTAGTGC	TCCTAGACGC	440
	CCCCGTGGGG	CTGGTGGCGC	GGTTGGCTGA	CGAGAGCGGC	480
	CACGTAGTGT	TGCGCTGGCT	CCCGCCGCCT	GAGACACCCA	520
15	TGACGTCTCA	CATCCGCTAC	GAGGTGGACG	TCTCGGCCGG	560
	CAACGGCGCA	GGGAGCGTAC	AGAGGGTGGA	GATCCTGGAG	600
	GGCCGCACCG	AGTGTGTGCT	GAGCAACCTG	CGGGGCCCGA	640
	CGCGCTACAC	CTTCGCCGTC	CGCGCGCGTA	TGGCTGAGCC	680
	GAGCTTCGGC	GGCTTCTGGA	GCGCCTGGTC	GGAGCCTGTG	720
20	TCGCTGCTGA	CGCCTAGCGA	CCTGGACCCC		750

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GATCGGATCC	ATGGGGTGGC	TTTGCTCTGG	GCTC	34
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(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:

56

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AGCTTCGAGC GGCCGCGTGC TGCTCGAAGG GCTCCCTGTA 40

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 696 base pairs
- 10 (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

	ATGGGGTGGC TTTGCTCTGG GCTCCTGTTC CCTGTGAGCT	40
15	GCCTGGTCCT GCTGCAGGTG GCAAGCTCTG GGAACATGAA	80
	GGTCTTGACAG GAGCCACCT GCGTCTCCGA CTACATGAGC	120
	ATCTCTACTT GCGAGTGGAA GATGAATGGT CCCACCAATT	160
	GCAGACCGGA GCTCCGCCTG TTGTACCAGC TGGTTTTTCT	200
	GCTCTCCGAA GCCCACACGT GSTATCCCTGA GAACAACGGA	240
20	GGCGCGGGGT GCGTGTGCCA CCTGCTCATG GATGACGTGG	280
	TCAGTGCGGA TAACTATACA CTGGACCTGT GGGCTGGGCA	320
	GCAGCTGCTG TGGAAGGGCT CCTTCAAGCC CAGCGAGCAT	360
	GTGAAACCCA GGGCCCCAGG AAACCTGACA GTTCACACCA	400
	ATGTCTCCGA CACTCTGCTG CTGACCTGGA GCAACCCGTA	440
25	TCCCCCTGAC AATTACCTGT ATAATCATCT CACCTATGCA	480
	GTCAACATTT GGAGTGAAAA CGACCCGGCA GATTTTCAGAA	520
	TCTATAACGT GACCTACCTA GAACCCTCCC TCCGCATCGC	560
	AGCCAGCACC CTGAAGTCTG GGATTTTCCTA CAGGGCACGG	600
	GTGAGGGCCT GGGCTCAGTG CTATAACACC ACCTGGAGTG	640
30	AGTGGAGCCC CAGCACCAAG TGGCACAACCT CCTACAGGGA	680
	GCCCTTCGAG CAGCAC	696

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(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 34 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GATCGAATTC ATGCTGGCCG TCGGCTGCGC GCTG

34

(2) INFORMATION FOR SEQ ID NO:14:

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
(B) nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

AGCTTCGAGC GGCCGCATCT TGCACTGGGA GGCTTGTCGC

40

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 1074 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

ATGCTGGCCG TCGGCTGCGC GCTGCTGGCT GCCCTGCTGG 40
25 CCGCGCCGGG AGCGGCGCTG GCCCAAGGC GCTGCCCTGC 80
GCAGGAGGTG GCAAGAGGCG TGCTGACCAG TCTGCCAGGA 120

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	GACAGCGTGA	CTCTGACCTG	CCCGGGGGTA	GAGCCGGAAG	160
	ACAATGCCAC	TGTTCACTGG	GTGCTCAGGA	AGCCGGCTGC	200
	AGGCTCCCAC	CCCAGCAGAT	GGGCTGGCAT	GGGAAGGAGG	240
	CTGCTGCTGA	GGTCGGTGCA	GCTCCACGAC	TCTGGAAACT	280
5	ATTCATGCTA	CCGGGCCGGC	CGCCCAGCTG	GGACTGTGCA	320
	CTTGCTGGTG	GATGTTCCCC	CCGAGGAGCC	CCAGCTCTCC	360
	TGCTTCCGGA	AGAGCCCCCT	CAGCAATGTT	GTTTGTGAGT	400
	GGGGTCCTCG	GAGCACCCCA	TCCCTGACGA	CAAAGGCTGT	440
	GCTCTTGGTG	AGGAAGTTTC	AGAACAGTCC	GGCCGAAGAC	480
10	TTCCAGGAGC	CGTGCCAGTA	TTCCCAGGAG	TCCCAGAAGT	520
	TCTCCTGCCA	GTTAGCAGTC	CCGGAGGGAG	ACAGCTCTTT	560
	CTACATAGTG	TCCATGTGCG	TCGCCAGTAG	TGTCGGGAGC	600
	AAGTTCAGCA	AAACTCAAAC	CTTTCAGGGT	TGTGGAATCT	640
	TGCAGCCTGA	TCCGCCTGCC	AACATCACAG	TCACTGCCGT	680
15	GGCCAGAAAC	CCCCGCTGGC	TCAGTGTAC	CTGGCAAGAC	720
	CCCCACTCCT	GGAATCATC	TTTCTACAGA	CTACGGTTTG	760
	AGCTCAGATA	TCGGGCTGAA	CGGTCAAAGA	CATTCAACAAC	800
	ATGGATGGTC	AAGGACCTCC	AGCATCACTG	TGTCATCCAC	840
	GACGCCTGGA	GCGGCCTGAG	GCACGTGGTG	CAGCTTCGTG	880
20	CCCAGGAGGA	GTTCTGGGCAA	GGCGAGTGGA	GCGAGTGGAG	920
	CCCGGAGGCC	ATGGGCACGC	CTTGGACAGA	ATCCAGGAGT	960
	CCTCCAGCTG	AGAACGAGGT	GTCCACCCCC	ATGCAGGCAC	1000
	TTACTACTAA	TAAAGACGAT	GATAATATTC	TCTTCAGAGA	1040
	TTCTGCAAAT	GCGACAAGCC	TCCCAGTGCA	AGAT	1074

25 (2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GATCGGATCC ATGCTGGGCA TCTGGACCCT CCTACC

36

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 42 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

AGCTTCGAGC GGCCGCGTTA GATCTGGATC CTTCTCTTT GC 42

(2) INFORMATION FOR SEQ ID NO:18:

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 519 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

ATGCTGGGCA TCTGGACCCT CCTACCTCTG GTTCTTACGT 40
CTGTTGCTAG ATTATCGTCC AAAAGTGTTA ATGCCCAAGT 80
GACTGACATC AACTCCAAGG GATTGGAATT GAGGAAGACT 120
GTTACTACAG TTGAGACTCA GAACTTGGA GGCCTGCATC 160
20 ATGATGGCCA ATTCTGCCAT AAGCCCTGTC CTCCAGGTGA 200
AAGGAAAGCT AGGGACTGCA CAGTCAATGG GGATGAACCA 240
GACTGCGTGC CCTGCCAAGA AGGGAAGGAG TACACAGACA 280
AAGCCCATT TTTCTTCCAAA TGCAGAAGAT GTAGATTGTG 320
TGATGAAGGA CATGGCTTAG AAGTGGAAT AACTGCACC 360
25 CGGACCCAGA ATACCAAGTG CAGATGTAAA CCAAACCTTT 400
TTTGTAATC TACTGTATGT GAACACTGTG ACCCTTGCAC 440
CAAATGTGAA CATGGAATCA TCAAGGAATG CAACTCACC 480
AGCAACACCA AGTGCAAAGA GGAAGGATCC AGATCTAAC 519

(2) INFORMATION FOR SEQ ID NO:19:

60

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

5

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GCCRCCATGG

10

Claims

1. A method of screening a plurality of compounds for the ability to bind a specific molecule comprising the steps:
 - 5 a) contacting one or more compound with a chimeric protein containing two or more distinct domains wherein a first domain comprises at least a portion of said specific molecule or a peptide analog thereof and a second domain contains at least a portion of an immunoglobulin chain
 - 10 having one or more region selected from the group consisting of:
 - i) an epitope, and
 - ii) a immunoglobulin region able to recognize an epitope,
 - 15 b) forming a binding partner complex between said chimeric protein and at least one of said compounds,
 - c) separating the complex from chimeric protein molecules not binding at least one compound,
 - d) contacting the binding partner complex with a
 - 20 directly or indirectly labeled secondary molecule able to bind the second domain of said chimeric protein, and
 - e) detecting said label as an indication of the presence of said compound.
2. The method of claim 1 wherein said first and
- 25 second domain of said chimeric protein are separated by an immunoglobulin heavy chain hinge region.
3. The method of claim 1 or 2 wherein said specific molecule is selected from the group consisting of:
 - a) an antigen,
 - 30 b) an antibody,
 - c) an enzyme,
 - d) an enzyme substrate,
 - e) a receptor, and
 - f) a ligand.

4. The method of claim 1 or 2 wherein said specific molecule is selected from the group consisting of: growth hormone, human growth hormone, bovine growth hormone, parathyroid hormone, thyroxine, insulin A-chain, insulin-B chain, proinsulin, relaxin A-chain, leptin receptor, fibroblast growth factor, relaxin B-chain, prorelaxin, follicle stimulating hormone, thyroid stimulating hormone, luteinizing hormone, glycoprotein hormone receptors, calcitonin, glucagon, factor VIII, an antibody, lung surfactant, urokinase, streptokinase, tissue plasminogen activator, bombesin, factor IX, thrombin, hemopoietic growth factor, tumor necrosis factor alpha, tumor necrosis factor beta, enkephalinase human serum albumin, mullerian-inhibiting substance, gonadotropin-associated peptide, β lactamase, tissue factor protein, inhibitin, activin, vascular endothelial growth factor, integrin receptors, thrombopoietin, protein A or D, rheumatoid factors, NGF- β , platelet growth factor, transforming growth factor, TGF- α , TGF - β , insulin-like growth factor I and II, insulin growth factor binding proteins, CD4, CD8, Dnase, Rnase, latency associated peptide, erythropoietin, osteoinductive factors, interferon-alpha, -beta and -gamma, colony stimulating factors, M-CSF, GM-CSF, G-CSF, stem cell factor, interleukins, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, superoxide dismutase, viral antigens, HIV envelope proteins, gp120, gp140, immunoglobulins, and proteins encoded by the Ig supergene family, and the naturally-occurring ligands or receptors of these compounds.

5. The method of claim 4 wherein said specific molecule comprises at least a portion of the tumor necrosis factor alpha receptor.

6. The method of claim 4 wherein said specific molecule comprises at least a portion of the endothelial growth factor receptor.

7. The method of claim 4 wherein said specific molecule comprises at least a portion of the thrombopoietin receptor.

8. The method of claim 4 wherein said specific
5 molecule comprises at least a portion of the TGF alpha receptor.

9. The method of claim 4 wherein said specific molecule comprises at least a portion of the TGF beta receptor.

10 10. The method of claim 4 wherein said specific molecule comprises at least a portion of the erythropoietin receptor.

11. The method of claim 4 wherein said specific molecule comprises at least a portion of the interferon
15 gamma receptor.

12. The method of claim 4 wherein said specific molecule comprises at least a portion of the GM-CSF receptor.

13. The method of claim 4 wherein said specific
20 molecule comprises at least a portion of the G-CSF receptor.

14. The method of claim 4 wherein said specific molecule comprises at least a portion of the IL-4 receptor.

25 15. The method of claim 4 wherein said specific molecule comprises at least a portion of the IL-6 receptor.

16. The method of claim 4 wherein said specific molecule comprises at least a portion of the leptin receptor.

17. The method of claim 4 wherein said specific
5 molecule comprises at least a portion of the fibroblast growth factor receptor.

18. The method of claim 2 wherein said first domain is positioned to the amino terminal side of said second domain on said chimeric protein.

10 19. The method of claim 2 wherein said first domain is positioned to the carboxy terminal side of said second domain on said chimeric protein.

20. The method of claim 18 wherein said immunoglobulin portion of said second domain comprises the C_H3
15 region of an immunoglobulin heavy chain.

21. The method of claim 20 wherein said immunoglobulin portion of said second domain comprises the C_H2 region of an immunoglobulin heavy chain.

22. The method of claim 1 or 2 wherein said com-
20 pounds are immobilized on a solid support.

23. The method of claim 1, 2 or 18 wherein said compounds comprise at least a portion of a chemical combinatorial library.

24. The method of claim 23 wherein said library is
25 comprised of members of the group selected of:

- a) naturally-occurring or non-naturally occurring amino acids,
- b) naturally-occurring or non-naturally occurring nucleotides,

c) naturally-occurring or non-naturally occurring saccharides, and

d) bi- or multifunctional small organic molecules.

25. The method of claim 22 wherein step c) is
5 accomplished by washing the solid support free of uncomplexed chimeric protein.

26. The method of claim 1 or 2 wherein said chimeric protein is produced by expression, within a host cell, of a recombinant DNA open reading frame encoding said
10 chimeric protein.

27. The method of claim 26 wherein said host cell expresses said chimeric protein as a dimer joined by at least one disulfide linkage, said dimer containing at least two specific binding partners.

15 28. The method of claim 22 wherein said compounds are contacted with bivalent chimeric protein dimers containing at least two specific binding partners.

29. The method of claim 26 wherein said host cell expresses DNA containing a second open reading frame
20 encoding a second chimeric protein, said second chimeric protein comprising a first domain containing at least a portion of said specific molecule or an analog thereof, and a second domain comprising at least a portion of an immunoglobulin chain having a region selected from the
25 group consisting of:

i) an epitope, and

ii) a immunoglobulin region able to recognize an epitope,

wherein said second chimeric protein contains at least a
30 portion of an immunoglobulin light chain.

30. The method of claim 29 wherein said chimeric protein and said second chimeric protein are comprised in a multimeric complex linked by at least one disulfide bond.

5 31. The method of claim 30 wherein the first domains of said chimeric protein and said second chimeric protein contain the same specific molecule portion or peptide analog thereof.

10 32. The method of claim 30 wherein the first domains of said chimeric protein and said second chimeric protein contain different specific molecule portions or peptide analogs thereof.

15 33. The method of claim 28 wherein at least one of said compounds are present in the form of a multimer, and said linked fusion protein dimer binds said compound more strongly than does a monomeric chimeric protein alone.

20 34. The method of claim 30 wherein at least one of said compounds are present in the form of a multimer and said multimeric complex binds said compound more strongly than do either said first or second chimeric protein alone.

35. The method of claim 26 wherein said host cell is a eukaryotic cell.

25 36. The method of claim 29 wherein said host cell is a eukaryotic cell.

37. The method of claim 26 wherein said open reading frame contains nucleotide sequences which direct the cell to add N-linked sugar residues to the chimeric protein expressed therefrom.

38. The method of claim 2 wherein said solid support is a cell.

39. The method of claim 2 wherein said solid support is a bacteriophage particle.

- 5 40. A method for screening one or more compounds for the ability to bind a specific molecule comprising the steps:
- 10 a) immobilizing to a solid support a chimeric protein containing two or more distinct domains wherein a first domain comprises at least a portion of said specific molecule or a peptide analog thereof and a second domain contains at least a portion of an immunoglobulin chain having a region selected from the group consisting of:
- 15 i) an epitope, and
- ii) a immunoglobulin region able to recognize an epitope,
- wherein said chimereic protein is immobilized to the solid support by an interaction between said solid support and said second domain,
- 20 b) contacting the immobilized chimeric protein with said compound or compounds to form a binding partner complex between the chimeric protein and compounds able to bind the specific molecule,
- c) washing said solid support to separate the
- 25 complex from chimeric protein molecules not binding at least one compound,
- d) detecting said chimeric protein as an indication of the presence of said compound.

30 41. The method of claim 40 wherein said first and second domain of said chimeric protein are separated by an immuoglobulin heavy chain hinge region.

42. The method of claim 41 wherein said first domain is positioned to the amino terminal side of said second domain on said chimeric protein.

43. The method of claim 41 wherein said first domain
5 is positioned to the carboxy terminal side of said second domain on said chimeric protein.

44. The method of claim 42 wherein said immunoglobulin portion of said second domain comprises the C_H3 region of an immunoglobulin heavy chain.

10 45. The method of claim 44 wherein said immunoglobulin portion of said second domain comprises the C_H2 region of an immunoglobulin heavy chain.

46. The method of claim 40 or 41 wherein said immobilized chimeric protein is in the form of a
15 disulfide-linked multimeric complex.

47. The method of claim 46 wherein said multimeric complex binds to two or more sites of said compound or compounds.

48. The method of claim 40 or 41 wherein said
20 compounds are comprised of members selected from the group consisting of:

- a) naturally-occurring or non-naturally-occurring amino acids,
- b) naturally-occurring or non-naturally-occurring
25 nucleotides,
- c) naturally-occurring or non-naturally occurring saccharides, and
- d) bi- or multifunctional small organic molecules.

49. The method of claim 40 wherein said chimeric
30 protein is immobilized by a binding interaction between

said chimeric protein and a moiety joined to the solid support selected from the group consisting of:

- a) an antigen,
- b) at least a portion of an antibody,
- 5 c) Protein G, and
- d) Protein A.

50. The method of claim 49 wherein said compound is eluted from said solid support before step d).

51. The method of claim 40 or 41 wherein the specific molecule is selected from the group consisting of:

- a) an antigen,
- b) an antibody,
- c) an enzyme,
- d) an enzyme substrate,
- 15 e) a receptor, and
- f) a ligand.

52. The method of claim 40 or 41 wherein said specific molecule is selected from the group consisting of: growth hormone, human growth hormone, bovine growth hormone, parathyroid hormone, thyroxine, insulin A-chain, insulin-B chain, proinsulin, relaxin A-chain, leptin receptor, fibroblast growth factor, relaxin B-chain, pro-relaxin, follicle stimulating hormone, thyroid stimulating hormone, luteinizing hormone, glycoprotein hormone receptors, calcitonin, glucagon, factor VIII, an antibody, lung surfactant, urokinase, streptokinase, tissue plasminogen activator, bombesin, factor IX, thrombin, hemopoietic growth factor, tumor necrosis factor alpha, tumor necrosis factor beta, enkephalinase human serum albumin, mullerian-inhibiting substance, gonadotropin-associated peptide, β lactamase, tissue factor protein, inhibitin, activin, vascular endothelial growth factor, integrin receptors, thrombopoietin, protein A or D, rheumatoid factors, NGF- β , platelet growth factor, transforming growth factor, TGF- α ,

TGF β , insulin-like growth factor I and II, insulin growth factor binding proteins, CD4, CD8, Dnase, Rnase, latency associated peptide, erythropoietin, osteoinductive factors, interferon-alpha, -beta and -gamma, colony stimulating factors, M-CSF, GM-CSF, G-CSF, stem cell factor, interleukins, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, superoxide dismutase, viral antigens, HIV envelope proteins, gp120, gp140, immunoglobulins, and proteins encoded by the Ig supergene family, and the naturally-occurring ligands, receptors, and/or substrates of these compounds.

53. A method of screening a compound for the ability to bind a specific binding partner comprising the steps:

a) constructing a recombinant DNA vector able to be expressed in a host cell, which vector comprises:

i) an open reading frame containing a first sequence region encoding at least a portion of an immunoglobulin chain which immunoglobulin chain contains one or more region selected from the group consisting of a region able to bind to an antigen, a region able to bind to an antibody, and an immunoglobulin-derived hinge region, and

ii) a promoter sequence positioned upstream of said open reading frame and able to direct RNA transcription of said open reading frame within said host cell,

wherein said open reading frame contains at least one restriction site located between said first sequence region and said promoter sequence for cloning a second nucleotide sequence region encoding at least a portion of a specific binding partner, provided said first and second nucleotide sequence region are cloned so as to preserve said open reading frame between said promoter sequence and a stop codon located not before the 3' end of said first nucleotide sequence region,

b) inserting said second nucleotide sequence into the vector at said restriction site,

- c) causing said vector to enter said host cell,
- d) incubating said host cell under conditions causing the expression of a chimeric protein containing the amino acids encoded by said first and second
5 nucleotide sequence,
- e) separating said chimeric protein from said host cell,
- f) contacting the compound with said chimeric protein under conditions favoring the binding of said
10 compound with said specific binding partner portion of the chimeric protein, and
- g) specifically detecting the presence of a bound fusion protein:compound complex as an indication of the presence of compounds able to bind said specific binding
15 partner.

54. The method of claim 53 wherein a third nucleotide sequence region encoding at least a portion of the hinge region of an immunoglobulin heavy chain is positioned between said first and second sequence region
20 so as to preserve said open reading frame between said promoter sequence and a stop codon located at or near the 3' end of said first nucleotide sequence region.

55. The method of claim 53 wherein said open reading frame encodes, upon expression, a chimeric protein containing two or more distinct domains wherein a first
25 domain comprises at least a portion of a specific binding partner and a second domain contains at least a portion of an immunoglobulin chain having a region selected from the group consisting of:

- 30 i) an epitope, and
- ii) a immunoglobulin region able to recognize an epitope.

56. The method of claim 55 wherein said specific binding partner will bind a member of the group consisting of:

- a) an antigen,
- 5 b) an antibody,
- c) an enzyme,
- d) an enzyme substrate,
- e) a receptor, and
- f) a ligand.

- 10 57. The method of claim 56 wherein said specific binding partner will bind at least a portion of a compound selected from the group consisting of: growth hormone, human growth hormone, bovine growth hormone, parathyroid hormone, thyroxine, insulin A-chain, insulin-B chain,
- 15 proinsulin, relaxin A-chain, leptin receptor, fibroblast growth factor, relaxin B-chain, prorelaxin, follicle stimulating hormone, thyroid stimulating hormone, luteinizing hormone, glycoprotein hormone receptors, calcitonin, glucagon, factor VIII, an antibody, lung surfactant,
- 20 urokinase, streptokinase, tissue plasminogen activator, bombesin, factor IX, thrombin, hemopoietic growth factor, tumor necrosis factor alpha, tumor necrosis factor beta, enkephalinase human serum albumin, mullerian-inhibiting substance, gonadotropin-associated peptide, β lactamase,
- 25 tissue factor protein, inhibitin, activin, vascular endothelial growth factor, integrin receptors, thrombopoietin, protein A or D, rheumatoid factors, NGF- β , platelet growth factor, transforming growth factor, TGF- α , TGF - β , insulin-like growth factor I and II, insulin growth factor
- 30 binding proteins, CD4, CD8, Dnase, Rnase, latency associated peptide, erythropoietin, osteoinductive factors, interferon-alpha, -beta and -gamma, colony stimulating factors, M-CSF, GM-CSF, G-CSF, stem cell factor, interleukins, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8,
- 35 IL-9, IL-10, IL-11, IL-12, superoxide dismutase, viral antigens, HIV envelope proteins, gp120, gp140, immuno-

globulins, and proteins encoded by the Ig supergene family, the naturally-occurring ligands, receptors, and/or substrates of these compounds, and analogs of these compounds, receptors and substrates thereof.

- 5 58. A method of screening a compound for the ability to bind a specific binding partner comprising the steps:
- a) constructing a recombinant DNA vector able to be expressed in a host cell, which vector comprises:
 - 10 i) an open reading frame containing a first sequence region encoding at least a portion of an immunoglobulin chain, and
 - ii) a promoter sequence positioned upstream of said open reading frame and able to direct RNA transcription of said open reading frame within said host cell,
 - 15 wherein said open reading frame contains at least one restriction site located at or near the 3' end of the first sequence region for cloning a second nucleotide sequence region encoding at least a portion of a specific binding partner, provided said first and second nucleotide
 - 20 sequence region are cloned so as to preserve said open reading frame between said promoter sequence and a stop codon located not before the 3' end of said second nucleotide sequence region,
 - b) inserting said second nucleotide sequence into
 - 25 the vector at said restriction site,
 - c) causing said vector to enter said host cell,
 - d) incubating said host cell under conditions causing the expression of a chimeric protein containing the amino acids encoded by said first and second
 - 30 nucleotide sequence,
 - e) separating said chimeric protein from said host cell,
 - f) contacting said compound with said chimeric protein under conditions favoring the binding of said
 - 35 compound with said specific binding partner portion of the chimeric protein, and

g) specifically detecting the presence of a bound fusion protein:compound complex as an indication of the presence of compounds able to bind said specific binding partner.

5 59. The method of claim 58 wherein a third nucleotide sequence region encoding at least a portion of the hinge region of an immunoglobulin heavy chain is positioned between said first and second sequence region so as to preserve said open reading frame between said promoter
10 sequence and a stop codon located at or near the 3' end of said second nucleotide sequence region.

 60. The method of claim 59 wherein said first nucleotide region open reading frame encodes, upon expression, a chimeric protein containing two or more distinct
15 domains wherein a first domain comprises at least a portion of a specific binding partner and a second domain contains at least a portion of an immunoglobulin chain having a region selected from the group consisting of:

- i) an epitope, and
- 20 ii) a immunoglobulin region able to recognize an epitope.

 61. The method of claim 60 wherein said first nucleotide sequence region encodes at least a portion of an immunoglobulin variable region.

25 62. The method of claim 60 or 61 wherein said specific binding partner portion will bind a member of the group consisting of:

- a) an antigen,
- b) an antibody,
- 30 c) an enzyme,
- d) an enzyme substrate,
- e) a receptor, and
- f) a ligand.

63. The method of claim 60 or 61 wherein said specific binding partner will bind at least a portion of a compound selected from the group consisting of: growth hormone, human growth hormone, bovine growth hormone, parathyroid hormone, thyroxine, insulin A-chain, insulin-B chain, proinsulin, relaxin A-chain, leptin receptor, fibroblast growth factor, relaxin B-chain, prorelaxin, follicle stimulating hormone, thyroid stimulating hormone, luteinizing hormone, glycoprotein hormone receptors, calcitonin, glucagon, factor VIII, an antibody, lung surfactant, urokinase, streptokinase, tissue plasminogen activator, bombesin, factor IX, thrombin, hemopoietic growth factor, tumor necrosis factor alpha, tumor necrosis factor beta, enkephalinase human serum albumin, mullerian-inhibiting substance, gonadotropin-associated peptide, β lactamase, tissue factor protein, inhibitin, activin, vascular endothelial growth factor, integrin receptors, thrombopoietin, protein A or D, rheumatoid factors, NGF- β , platelet growth factor, transforming growth factor, TGF- α , TGF - β , insulin-like growth factor I and II, insulin growth factor binding proteins, CD4, CD8, Dnase, Rnase, latency associated peptide, erythropoietin, osteoinductive factors, interferon-alpha, -beta and -gamma, colony stimulating factors, M-CSF, GM-CSF, G-CSF, stem cell factor, interleukins, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, superoxide dismutase, viral antigens, HIV envelope proteins, gp120, gp140, immunoglobulins, and proteins encoded by the Ig supergene family, the naturally-occurring ligands, receptors, and/or substrates of these compounds, and analogs of these compounds, receptors and substrates thereof.

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US97/05821

A. CLASSIFICATION OF SUBJECT MATTER

IPC(6) : G01N 33/53, 33/543; C12N 15/00; C12Q 1/00, 1/68, 1/70

US CL : Please See Extra Sheet.

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 435/4, 5, 6, 7.1, 7.2, 7.21, 7.92, 69.1, 69.3, 69.4, 69.5, 69.7, 172.2, 172.3, 320.1; 436/518; 935/80, 81

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched
NoneElectronic data base consulted during the international search (name of data base and, where practicable, search terms used)
Please See Extra Sheet.

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	US 5,338,665 A (SCHATZ et al) 16 August 1994, entire document, especially abstract, column 5, line 16 to column 8, line 57, column 12, line 56 to column 13, line 3.	1-63
X	US 5,432,018 A (DOWER et al) 11 July 1995, entire document, especially abstract, column 1, line 59 to column 2, line 58, column 4, lines 10-42, column 5, line 13 to column 6, line 53, claims 3-12.	1-63
A	HOUGHTEN et al. Generation and use of synthetic peptide combinatorial libraries for basic research and drug discovery. Nature. 07 November 1991, Volume 354, pages 84-86.	1-63

☒ Further documents are listed in the continuation of Box C.
 ☐ See patent family annex.

* Special categories of cited documents:	
A document defining the general state of the art which is not considered to be of particular relevance	*T* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
E earlier document published on or after the international filing date	*X* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
L document which may throw doubt on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	*Y* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
O document referring to an oral disclosure, use, exhibition or other means	*Z* document member of the same patent family
P document published prior to the international filing date but later than the priority date claimed	

Date of the actual completion of the international search

14 JULY 1997

Date of mailing of the international search report

25 JUL 1997

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INTERNATIONAL SEARCH REPORT

International application No.
PCT/US97/05821

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	TANABE et al. Structural and functional analysis of monomorphic determinants recognized by monoclonal antibodies reacting with the HLA class α_3 domain. J. Immunol. 15 May 1992, Volume 148, No. 10, pages 3202-3209.	1-63
A	SHIN et al. Transferrin-antibody fusion proteins are effective in brain targeting. Proc. Soc. Natl. Acad. Sci. USA. March 1995, Volume 92, pages 2820-2824.	1-63

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US97/05821

A. CLASSIFICATION OF SUBJECT MATTER:

US CL :

435/4, 5, 6, 7.1, 7.2, 7.21, 7.92, 69.1, 69.3, 69.4, 69.5, 69.7, 172.2, 172.3, 320.1; 436/518; 935/80, 81

B. FIELDS SEARCHED

Electronic data bases consulted (Name of data base and where practicable terms used):

APS, CAS ONLINE

search terms: chimeric proteins, fusion proteins, epitopes, immunoglobulin, antigen, antibody, label, library, screening, enzymes, vectors, receptors, recombinant DNA, biotin, avidin, streptavidin